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Best Local Similarity
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                                                                                         121 ATCGGGTGGATGCCGGTGGCCAACTGCCCCATGCCCCTGGCCCCGGCCGACAAGAACAAG
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Sequence 1 from patent US 6395477.
AR371346
AR371346.1 GI:34608278
                                                                                                                                                                                              1 GATTTGCTGAACTAACTCCAAGCTGGTGTGCCTAGCGTCCGCGGCGGCTGCCGGCCCAAGA
                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 2121)

Cockett,M.I., Dilks,D.W., Ling,H.-P.C. and Sokol,P.T.

Human potassium channel polynucleotide and polypeptides
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                                                                                                                                          GCTGGAGTCACCATGGCGGCCGGAGTTGCGGCCTGGCTTTTGCCCCGGGCTGCGGCC
                                                                                                                                                                               GATTTGCTGAACTAACTCCAAGCTGGTGTGCCTAGCGTCCGCGCGGCTGCCGGCCCAAGA
                                        CGGCAGGATGAGCTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACC
                                                                           ATCGGGTGGATGCCGGTGGCCAACTGCCCCATGCCCCTGGCCCGGCCGACAAGAACAAG
                                                                                                                             ACGCTGGAGCGCTACCCGGACACCCTGCTGGGCAGCACGGAGAAGGAGGTTCTTCTTCAAC
                         CGGCAGGATGAGCTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACC
                                                                                                                                                                                                                                100.0%; Score 2121; illarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                        US 6395477-A 1 28-MAY-2002;
Location/Qualifiers
1. .2121
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/mol_type="genomic DNA"
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1081 ACTGTGATGTTTTATGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCCTGCC 1140	11 AGGTGGAAGGCTACCCGGACACCCGGCACACGGAAAAAGGATTCTTCTCTCAAC 300  21 AAGGACACCAAGGAATACTTCTTCGACCGGACACCGAAAAAAAA
RESULT 2 AF120491 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	
AF120491  AF120491  Homo sapiens Shal-related potassium channel Kv4.3 (KCND3) mRNA, long splice variant, complete cds.  AF120491  AF120491.1 GI:5059059  Homo sapiens (human)  Homo sapiens  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 2722)  Isbrandt,D., Leicher,T., Waldschutz,R., Zhu,X., Luhmann,U., Michel,U., Sauter,K. and Pongs,O.  Gene structures and expression profiles of three human KCND (Kv4) potassium channels mediating A-type currents I(TO) and I(SA)  Genomics 64 (2), 144-154 (2000)	1321 GATAAACGAGGGCAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAACAGGCT 1380 1381 AGTTCGAATGCATACCTGCACCAGCAAGGCCAGCCACCAGAGCTCCTCACGAACGA

Qy db	Db Qy	g 49	Qy Db	P Q	Qy dd	Qy Db	Qy Db	Query Ma Best Loc Matches	ORIGIN				CDS	gene		JOURNAL	MEDLINE PUBMED REFERENCE AUTHORS
421 GAGCTGGCCTTCTACGGCATCCTCCCCGGAGATCATCGGGGACTGCTGCTACGAGGAGTAC 480	361 TTCTACCGCACGGGGAAGCTGCACTACCCCGCGCTACGAGTGCATCTCTGCCTACGACGAC 420	301 GAGGACACCAAGGAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAAC 360	241 ACGCTGGAGCGCTACCCGGACACCCTGCTGGGCAGCACGGAGAAGGAGTTCTTCTTCAAC 300	181 CGGCAGGATGAGCTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACC 240	121 ATCGGGTGGATGCCGGTGGCCAACTGCCCCATGCCCCTGGCCCGGCCGACAAGAACAAG 180 537 ATCGGGTGGATGCCGGTGGCCCAACTGCCCCATGCCCCTGGCCCGGCCGACAAGAACAAG 596	1	1 GATTTGCTGAACTAACTCCAAGCTGGTGTGCCTAGCGTCCGCGCGGCTGCCGGCCCAAGA 60	Match 96.0%; Score 2036.2; DB 9; Length 2722; Local Similarity 97.5%; Pred. No. 1.2e-306; Les 2068; Conservative 0; Mismatches 53; Indels 0; Gaps 0;	PEGESRPPPASPGPNTNIPSITSNVVKVSVL"	GERTS VAR F CLUITAC VMITE I GETTIKKLE AAFSKI KE I KS VMS I LIVV KARET I I GETM TINEDVSGAFVTLKVFRVFRI FKFSRHSGELRI LGYTLKSCASELGFLLFSLTMAI I I FATVMFYAEKGSSASKFTS I PASFWYTI VTMTTLGYGDMVLKTI AGKI FGSI CSLSGV LVI ALPVPVI VSNFSR I YHQNQRADKRRAQKKARLAK I RVAKTGSSNAYLHSKRNGLL NGAI EI TCTDEGGELMCKTTTG I EGGLUHLI I UGI EKTTTG I SVI UDDDI I GUTTGTI KNIJ	NVSGRRFQTWRTTLERY POTILIFE AKAMAH GWIFE VAN CETE WAT FILDNING DE LI VE NVSGRRFQTWRTTLERY POTILIGSTEKEFFFINEDTKEYFFDRDEVFRCVILNFYRTGK LHYPRYECISAYTDELAFYGILIGECCYEEYKDRKRENAERLMDDNDSENNQESM PSLSFRQTWRAFENPHTSTLALVFYYVTGFFINGVNGTTNUNGTTNUNGTUND	/codon_start=1 /product="Sha1-related potassium channel Kv4.3" /protein_id="AAD38898.1" /protei="GI:5059060" /db_xref="GI:5059060"	/gene="KCND3" /gene="KCND3" /note="long splice variant"	/map="1p13" /tissue_type="cortex" 12722	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /chromosome="1"	Submitte Signalve	20195625 10729221 2 (bases 1 to 2722) 3 Zhu,X.R., Waldschuetz,R., Isbrandt,D., Sauter,K. and Pongs,O.
₽ <b>Q</b>	) B 8	S & &	) 당 성	B &	Db Qy	B 8	dg Vy	₽ <b>₹</b>	B 8	Qy dd	ρ <i>Q</i> γ	D	QQ da	B Q	Db Qy	B 8	D Q
1501 CATCACCTGCTGCACTGCCTGGAAAAAACCACTGGGTTGTCCTATCTTGTGGATGATCCC 1500	*1 ACGGGCACCCCAGAAGAGGGCACATIGGGCAAGACCACCTCACTCATCGAGAGCCAGCAT 190 57 ACGGGCACCCCAGAAGAGGAGCACATGGGCAAGACCACCTCACTCA	81 AGECCACACACACACACACACACACACACACACACACACA	321 GATAAACGCAGGCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCAAAACAGGC 13	261 CTGCCAGTCCCTGTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAAACCT 132 [	01 ACGATTGCAGGGAAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCATTGCC 126	41 TCGTTTTGGTACACCATTGTCACCATGACCACACTGGGATACGGAGACATGGTGCCTAAG 120	SGCTCCTCGGCCAGCAAGTTCACAAGCATCCCTGCC 114 	021 IGIGCTCCGAACIGGCTTTCTTCTCTCTCTCCCTCACCATGGCCATCATCATCTTTGCC 108 [	961 ATCTTCAAGTTTTCCCGCCACTCCCAGGGCCTGCGGATCCTGGGCTACACACTGAAGAGC 102	901 ACCAACAACGAGGACGTGTCCGGCGCCTTCGTCACGCTCCGGGTCTTCCGCGTCTTCAGG 960 	841 AGCGTCATGAGCATCATCGACGTGGTGGTCATCATGCCCTACTACATCGGTCTGGTCATG 900	781 TTCACCGTGGAGTACCTCCTGCGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCATCCGC 840	721 CCGTGCGGGGAGCGCTACTCGGTGGCCTTCTTCTGCCTGGACACGGCGTGCGT	661 GTCATCACCAACGTGGTGGAGACGGTGCCGTGCGGCACGGTCCCGGGCAGGAGGAGCTG 720	601 CACACCAGCACGCTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTCG 660	541 CAGGAGTCCATGCCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGGCCTTCGAGAACCCC 600	481 AAGGACCGCAAGAGGGAGAACGCCGAGCGGCTCATGGACGACAACGACTCGGAGAACAAC 540 

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Direct Submission
Submitted (17-SEP-1999) Neuroscience, Wyeth-Ayerst Research,
8000, Room 1119A, Princeton, NJ 08543-8000, USA
Location/Qualifiers
1. .2041
                                                                                                                                                                                                                                                                                                                                                                                      2041 bp mRNA linear Homo sapiens voltage gated potassium channel Kv4.3 variant (Kv4.3) mRNA, complete cds. AF187963.1 GI:6007794
                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                      1 (bases 1 to 2041)
Dilks,D., Ling,H.P., Cockett,M., Sokol,P. and Numann,R.
Cloning and expression of the human kv4.3 potassium chan
J. Neurophysiol. 81 (4), 1974-1977 (1999)
                                                                                                                                                                                         2 (bases 1 to 2041)
Dilks, D.W., Ling, H.-P.,
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Homo sapiens
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1. .2041
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73. .2040
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                                                 GTCATCACCAACGTGGTGGAGACGGTGCCGTGCGGCACGGTCCCCGGGCAGCAAGGAGCTG
                                                                                                                CACACCAGCACGCTGGCCCTGGTCTTCTACTACGTGACTGGCTTTCTTCATCGCTGTCTCG
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CAGGAGTCCATGCCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGGCCTTCGAGAACCCC
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splice variant"
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EFIDEQMFEQNCMESSMQNYPSQRSPSLSSHPGLTTTCCSRRSKKTTHLPNSNLPDTR
LRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDGLRPNCKTSQITTAIISIPTPPALT
PEGESRPPPASPGPNTNIPSIASNVVKVSVL"
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CACATCCAGGGCAGTGAGCAGCCCTCCCTCACAACCAGTCGCTCCAGCCTTAATTTGAAA
                                                                             CATCACCTGCTGCACTGCCTGGAAAAAACCACTGGGTTGTCCTATCTTGTGGATGATCCC
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                                             CTGCCCAATTCTAACCTGCCAGCTACTCGCCTGCGCAGCATGCAAGAGCTCAGCACGATC
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1 (bases 1 to 2064)

Cockett, M.I., Dilks, D.W., Ling, H.-P.C.
Human potassium channel polynucleotide
thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent: US 6395477-A 3 28-MAY-2002;
Location/Qualifiers
1. .2064
                                                                                 GAGGACACCAAGGAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAAC 360
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                                         TTCTACCGCACGGGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGAC
                                                                                                                                                                                                 CGGCAGGATGAGCTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACC
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ilarity 97.3%;
Conservative
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from patent US 6395477.
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Pred. No. 1.6e-300;
0; Mismatches 0;
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REFERENCE 1 (bases 1 t AUTHORS Kong, W. and TITLE Direct Submit	1261 CTGCCAGTCCCTGTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAGAGGCT 1320 	A 4
SOURCE Homo sapiens ORGANISM Homo sapiens Eukaryota; Me	1201 ACGATTGCAGGGAAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCATTGCC 1260	8 8
	1141 TCGTTTTGGTACACCATTGTCACCATGACCACACTGGGATACGGAGACATGGTGCCTAAG 1200	д Q
RESULT 5 AF048713 LOCUS AF048713 DEFINITION Homo sapiens	1081 ACTGTGATGTTTTATGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCCTGCC 1140	B 8
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1804	781 TTCACCGTGGAGTACCTCCTGCGGGCTCTTCGCGGGCTCCCAGCCGCTACCGCTTCATCCGC 840	용 성
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ACCESSION
AF048713.1 GI:2935435

KEYWORDS
SOURCE
SOURCE
CORGANISM
Homo sapiens (human)
CORGANISM
Homo sapiens (human)
CORGANISM
Homo sapiens
Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
TITLE
JOURNAL
Of Medicine, 720 Rutland Avenue, Ross 844, Baltimore, MD 21205, USA
FEATURES

BOURCE

OF Medicine, 720 Rutland Avenue, Ross 844, Baltimore, MD 21205, USA
FEATURES

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OF Medicine, 720 Rutland Sepiens

(homo sapiens

1.1968

Organism="Homo sapiens"

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Pred. No. 2.8e-295;
0; Mismatches 3;
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433 TACGGCATCCTCCCGGAGATCATCGGGGACTGCTGCTACGAGGAGTACAAGGACCGCAAG 492	313 GAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTTCTACCGCACG 372	193 CTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACCACGCTGGAGCGC 252	73 ATGGCGGCCGAAGTTGCGGCCTGGCTGCCTTTTGCCCCGGGCTGCGGCCATCGGGTGGATG 132	/mol_type="unassigned DNA" /mol_type="unassigned DNA" /db_xref="taxon:32644"  Match 92.5%; Score 1962; DB 6; Length 2072; ocal Similarity 99.7%; Pred. No. 4.2e-295; s 1965; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	unclassified.  E 1 (bases 1 to 2072)  E 1 (bases 1 to 2072)  IS Bril,A.M. and Calmels,T.P.  KV POTASSIUM CHANNEL POLYPEPTIDES AND POLYNUCLEOTIDES  L Patent: WO 9842833-A 3 01-OCT-1998;  BRIL ANTOINE MICHEL ALAIN (FR); CALMELS THIERRY PAUL GERARD (FR)  Location/Qualifiers  1. 2072  1. 2072	A85166 2072 bp DNA linear PAT 21-JAN-2000 ON Sequence 3 from Patent WO9842833. N A85166 A85166.1 GI:6733868 unidentified SM unidentified	
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2072 bp DNA linear PAT CUS AR204885 AR204885 AR204885 CESSION AR204885.1 GI:21502325 WORDS UNCHAOME. DRAWNISM UNCLASSIFIED. ANTHORS FRINTE LOGANISM UNCLASSIFIED. ANTHORS FAIVE, JF. Simon. Pierre., Javre, JL. and Rouanet, S. Faive, JF. Simon. Pierre., Javre, JL. and Rouanet, S. TURES FOURNAL LOGATION, COALINE, JF. Simon. Pierre., Javre, JL. and Rouanet, S. TURES FAIVE, JF. Simon. Pierre., Javre, JL. and Rouanet, S. TURES FOURNAL LOGATION, COALIFIED BE 6; Length 2072; Desting The Local Similarity 99.7%; Pred. No. 4. 2e-295; Desting The Local Similarity 99.7%; Pred. No. 4. 2e-295; Desting The Local Similarity 99.7%; Pred. No. 4. 2e-295; Desting The Local Similarity 109.7%; Pred. No. 4. 2e-295; Desting The Coargeogacagaagaagaagaagaagaagaagaagaagaagaagaa	Qy  1753 AACCTGCCAGCTACTCGCCTGCGCAGCATGCAAGAGCTCAGCACGATCCAGGGC 1812
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	CGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACCACC	Qy 133 CCGGTGGCCAACTGCCCCATGCCCCTGGCCCGGCCGAAGAACAAGCGGCAGGATGAG	73 AIGGCGGCCGAGTIGCGGCCIGGCTGCCTTTTGCCCGGGCTGCGGCCAICGGGTGG 	Query Match 92.4%; Score 1960; DB 6; Length 1968; Best Local Similarity 99.7%; Pred. No. 8.7e-295; Matches 1963; Conservative 0; Mismatches 5; Indels 0; Gaps		nt: WO 03097682-A 4 27-NOV-2003; en NV (BE) Location/Qualifiers 11968	T.J., Dewulf, N.E. and Plaetinck, G.K. for identifying and developing compounds that gated potassium channels of the kv4 family	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	4 from Patent W003097682.	AX956786 1968 bp	QY 1993 AACATTCCTTCCATAACCAGCAATGTTGTCAAGGTCTCTGTCTTGTAAAA 2042	QY 1933 CCAGCGCTAACCCCCAGAGGGGGAAAGTCGGCCACCCCCTGCCAGCCCCAGGCCCCAACACGC	QY 1873 CTGAGACCAAAACTGCAAAACATCCCAGATCACCACAGCCATCATCAGCATCCCCACTCCCC	QY 1813 AGTGAGCAGCCCTCCCTCACAACCAGTCGCTCCAGCCTTAATTTGAAAGCAGACGACGACGACGACGACGACGACGACGACGAC	QY 1753 AACCTGCCAGCTACTCGCCTGCGCAGCATGCAAGAGCTCAGCACGATCCACATCCAGGGC	Qy 1693 GGCCTCACTACCACCTGCTGCTCCCGTCGTAGTAAGAAGACCACACACCCCGAATTCT	Qy 1633 ATGGAGAGTTCAATGCAGAACTACCCATCCACAAGAAGTCCCTCACTGTCCAGCCACCCA	QY 1573 CGAACCTCCACCATCAAGAACCACGAGTTTATTGATGAGCAGATGTTTGAGCAGAACTGC
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 2 (bases 1 to 1968)
Direct Submission
Submitted (17-NOV-1999) Cardiovascular Pharmacology,
Beecham, 4 Rue du Chesnay Beauregard, Saint Gregoire
Location/Qualifiers
                                                                                                                                                                                                                                       Homo sapiens potassium complete cds.
AF205857
                                                                                    Long and Short Human Isoforms Expression, Electrophysiology, Protein Kinase C
                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1968)

Calmels, T. P. G., Faivre, J.-F., Javre, J.-L., Cheval, B., Rouanet, S. and Bril, A.
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                                                                           CTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTCGGTCATCACCAAC
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NVSGRRFQTWRTTLERYPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGK
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PSLSFRQTWWRAFENPHTSTLALVFYYVTGFFIAVSVITNVVETVPCGTVPGSKELPC
GERYSVAFFCLDTACVMIFTVEYLLRLFAAPSRFRFIRSVMSIIDVVAIMPYYIGLVM
TNNEDVSGAFVTLRVFRVFRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIII
FATVMFYAEKGSSASKFTSIPASFWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLGGV
LVIALPYPVIVSNFSRIYHQNQRADKRRAQKKARLARIRVAKTGSSNAYLHSKRNGLL
NEALELTGTPEEEHMGKTTSLIESQHHHLLHCLEKTTGLSYLVDDPLLSVRTSTIKNH
EFIDEQMFEQNCMESSMQNYPSTRSPSLSSHPGLTTTCCSRRSKKTTHLPNSNLPATR
LRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDGLRPNCKTSQITTAIISIPTPPALT
PEGGESRPPPASPGPNTNIPSIASNVVKVSAL"
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/protein_id="AAF20925.1"
/db_xref="GI:6644152"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae;
1 (bases 1 to 1984)
Dilks,D., Ling,H.P., Cockett,M., Sokol,P. and Numann,
Cloning and expression of the human kv4.3 potassium of J. Neurophysiol. 81 (4), 1974-1977 (1999)
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Homo sapiens voltage gated potassium
variant (Kv4.3) mRNA, complete cds.
AF187964
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Direct Submission
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GERYSVAFFCLDTACVMIFTVEYLLRLFAAFFIRVFIRSVMSIIDVVAIMPYYIGLVM
TNNEDVSGAFVTLRVFRVFRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIII
FATVMFYAEKGSSASKFTSIPAFFWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGV
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NGALELTGTPEEEHMGKTTSIPAFFWYTIVTHLFNSNLPDTRLRSMQELSTIHIQGSEQPS
LTTSRSSLNLKADDGLRPNCKTSQITTAIISIPTPPALTPEGESRPPPASPGPNTNIP
SIASNVVKVSVL"
                                                                                                                                                                                                                                                           /gene="Kv4.3"
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TTGAGTGGCGTCCT	SULT 11 048712 AF048712 1911 bp mRNA linear CUS AF048712 Homo sapiens Kv4.3 potassium channel short splice mRNA, complete cds.	

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AF048712.1
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1 (bases 1 to 1911)

Kong, W. and Tomaselli, G.F.

Direct Submission
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TACCCGGACACCCTGCTGGGCAGCACGAGAAGGAGTTCTTCTTCAACGAGACACCAAG
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                                                                       GGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGACGAGGTGGCCTTC
                                                                                                               GAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTTCTACCGCACG
                                                                                                                                GAGTACTTCTTCGACCGGGGACCCCGAGGTGTTCCGCCTGCGTGCTCAACTTCTACCGCACG
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PSLSFRQTWWRAFENPHTSTLALVFYYVTGFFIAVSVITNVVETVPCGTVPGSKELPC
GERYSVAFFCLDTACVMIFTGEYLLRLPAAPSRYRFIRSVMSIIDVVAIMPYYIGLVM
TNNEDVSGAFVTLRVFRVFRIFKESRHSQGLRLGSTTLGYTLKSCASELGFLLFSLTMAIII
FATVMFYAEKGSSASKFTSIPASFWYTIVTMTTLGYGDMVLKTIAGKIFGSICSLGV
LVIALPVPVIVSNFSRIYHQNQRADKRRAQKKARLARIRVAKTGSSNAYLHSKRNGLL
NEALELTGTPEEEHMGKTTSLIESQHHHLLHCLEKTTNHEFIDEQMFEQNCMESSMON
YPSTRSPSLSSHPGLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPS
LTTSRSSLNLKADDGLRPNCKTSQITTAIISIPTPPALTPEGESRPPPASPGPNTNIP
SITSNVVKVSVL"
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                                                                                                                            TACCTGCACAGCAAGCGCAACGGGCTCCTCAACGAGGCGCTGGAGCTGACGGCCACCCCA
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                                       CACTGCCTGGAAAAAACCACTGGGTTGTCCTATCTTGTGGATGATCCCCTGTTATCTGTA
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Qy	Db Qy	D Q	Qy Db	Query Best Matcl	Origin	JOURNAL	REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	A85164 LOCUS DEFINITION ACCESSION	Db RESIT.T 10	Q	Qy Db	Db Qy	ду У	Db Qy	Db	Q b	. Q E	Dy Qy
253 TACCCGGACACCCTGCTGGGCAGCACGGAGAAGGAGTTCTTCTTCAACGAGGACACCAAG 312	GTTCCAGACCTGGAGGACCACGCTGGAGCGC 2 	133 CCGGTGGCCAACTGCCCCATGCCCCTGGCCCCGGCCAAAGAACAAGCAGCGGCAGGATGAG 192	73 ATGGCGGCCGAGTTGCGGCCTGGCTGCCTTTTGCCCGGGCTGCGGCCATCGGGTGGATG 132	/ Match 86.7%; Score 1838; DB 6; Length 2104; Local Similarity 96.4%; Pred. No. 7.7e-276; nes 1914; Conservative 0; Mismatches 15; Indels 57; Gaps 1;	G	Patent: WO 9842833-A 1 01-OCT-1998; BRIL ANTOINE MICHEL ALAIN (FR); CALMELS THIERRY PAUL Location/Qualifiers	x 80 12 12		A85164 2104 bp DNA linear PAT 21-JAN-2000 ON Sequence 1 from Patent WO9842833.	64	993 AACATTCCTTCCATAACCAGCAATGTTGTCAAGGTCTCTGTCTTGTAA 2040	1933 CCAGCGCTAACCCCAGAGGGGGAAAGTCGGCCACCCCTGCCAGGCCCAGGCCCCAACACG 1992	1873 CTGAGACCAAACTGCCAAAACATCCCAGATCACCACAGCCATCATCAGCATCCCCACTCCC 1932	1813 AGTGAGCAGCCCTCCCCACAACCAGTCGCTCCAGCCTTAATTTGAAAGCAGACGACGACGGA 1872	1753 AACCTGCCAGCTACTCGCCTGCGCAGCATGCAAGAGCTCAGCACGATCCACATCCAGGGC 1812	564 GGCCTCACTACCACCTGCTGCTCCCGTCGTAGTAAGAAGACCACACACCTGCCCAATTCT 162	1504 ATGGAGAGTTCAATGCAGAACTACCCATCCACAAGAAGTCCCTCACTGTCCAGCCACCCA 1563 1693 GGCCTCACTACCACCTGCTGCTCCCGTCGTAGTAAGAAGACCACACACCTGCCCCAATTCT 1752	633 ATGGAGAGTTCAATGCAGAACTACCCATCCACAGAAGTCCCTCACTGTCCAGCCACCCA 169	573 CGAACCTCCACCATCAAGAACCACGAGTTTATTGATGAGCAGATGTTTGAGCAGAACTGC 16
DB QY	do Qy	Db G	D Dy	Qy Db	DB 99	B 8	Qy dd	. da	g 82	Qy dd	D .	δ β	<i>S</i> y B	Qy Qy	S S	, Qy	g dy	B &	g. Db
1333 GCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAACAGGCAGTTCGAATGCA 1392 	73 GTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAGAGCTGATAAACGCAGG 133	13 AAGATOTTOGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCATTGCCCTGCCAGTCCCT 120	153 ACCATTGTCACCATGACCACACTGGGATACGGAGACATGGTGCCTAAGACGATTGCAGGG 121	93 TATGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCCTGCCTCGTTTTGGTAC 115 	1033 CTGGGCTTTCTTCTCTCCCCTCACCATGGCCATCATCATCTTTTGCCACTGTGATGTTT 1092	973 TCCCGCCACTCCCAGGGCCTGCGGATCCTGGGCTACACTGAAGAGCTGTGCCTCCGAA 1032	913 GACGIGICCGGCGCCTTCGTCACGCTCCGGGTCTTCCGCGTCTTCAGGATCTTCAAGTTT 972	853 ATCATCGACGTGGTGGCCATCATGCCCTACTACATCGGTCTGGTCATGACCAACAACGAG 912	793 TACCTCCTGCGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCATCCGCAGCGTCATGAGC 852	733 CGCTACTCGGTGGCCTTCTTCTGCCTGGACACGGCGTGCGT		1 CTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTCGGTCAT	1 cccrcgcrcAgcrrccgccAgAccArgrggcgggccrrcGAgAAcccccAcAccAgcAc	1 AGGGAGAACGCCGAGCGGCTCATGGACGACGACGACGAGGAGAACAACCAGGAGTC 3 CCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGGCCTTCGAGAACCCCCACACCAC 1	1 TACGGCATCCTCCCGGAGATCATCGGGGACTGCTGCTACGAGGAGTACAAGGACCGCAAG 4 3 AGGGAGAACGCCGAGCGAGCGCTCATGGACGACGACTCCGGAGAACAACCAGGAGTCCATG 5	3 TACGGCATCCTCCCGGAGATCATCGGGGGACTGCTGCTACGAGGAGTACAAGGACCGCAAG 49	373 GGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGACGAGCTGGCCTTC 432	GAGIACIICIICGACCGGGACCCCGAGGIGIICCGCGGGGGGCTCAACIICIACGCACG 30	1 TACCCGGACACCCTGCTGGGCAGCACGGAGAAGGAGTTCTTCTTCAACGAGGACACCAAG 24

Db 1624 AACCTGCCAGCTACTGCGCAGCANGCAAGAGCTCAGACGANTCCACATCCAGGGC 1683  Oy 1813 AGTGAGCAGCCCTCCCTCACAACCAGTGCTCAGCCTCTCAATTTGAAAGAGCCAAGCGAACCAGCCCTCACAACCTCCACAACCAGCCCTCAAATTGCAAAACCAGTCCCACAACCACCACACCACACCACACCACACCACACCCCACA	1393 TACCTGCACAGCAAGCGCAACGGGCTCCTCAACGAGGCGCTGGAGGTGACGGGCACCCCA 145
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Submitted (17-NOV-1999) Cardiovascular Pharmacology, SmithKline
Beecham, 4 Rue du Chesnay Beauregard, Saint Gregoire 35760, France
Location/Qualifiers
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1911)
Calmels, T.P.G., Faivre, J.-F., Javre, J.-L., Cheval, B., Rouanet, S.
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Calmels, T.P.G., Faiv
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      TACGGCATCCTCCCGGAGATCATCGGGGGACTGCTACGAGGAGTACAAGGACCGCAAG
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YPSTRSPSLSSHPGLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPS
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Pred. No. 1.6e-275;
0; Mismatches 5;
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193 C	1381 GAAGAGGAGCACATGGGCAAGACCACCTCACTCATCGAGAGCCAGCATCATCATCACCTGCTG 144	당 성
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Db 1 ATGGC	Y 1393 TACCTGCACAGCAAGCGCAACGGGCTCCTCAACGAGGCGCTGGAGCTGACGGGCACCCCA 1452	용 성
Qy 73 ATGGCC		망
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JOURNAL Patent: BRIL ANT	1081 ACCATTGTCACCACGCACACTGGGATACGGAGACATGGTGCCTAAGACGATTGCAGGG 1140	문 성
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M	/ 1093 TATGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCCTGCCTTCGTTTTGGTAC 1152	ફ
ACCESSION A85168.1 VERSION A85168.1 KEYWORDS	/ 1033 CTGGGCTTTCTTCTCTCCCTCACCATGGCCATCATCATCTTTTGCCACTGTGATGTTT 1092	음 성
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1624	673 GIGGIGGAGACGGIGCCGTGCGGCACGGTCCCGGGCAGCAAGGAGCTGCCGTGCGGGAG 7	Ş
Ov 1753 AACCTO	541 CTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTCGGTCATCAC	ઠ
1564	613 CTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTCGGTCATCACCAA	8
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1462	493 AGGGAGAACGCCGAGCGGCTCATGGACGACGACGACTCGGAGAACAACCAGGAGTCCCATG 5	\$ 8
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POTASSIUM CHANNEL POLYPEPTIDES AND POLYNUCLEOTIDES
ent: WO 9842833-A 5 01-OCT-1998;
L ANTOINE MICHEL ALAIN (FR); CALMELS THIERRY PAUL GER
Location/Qualifiers
                                                                                                                                                         86.3%; Score 1830; DB 6; Length 2104; arity 96.1%; Pred. No. 1.3e-274; onservative 0; Mismatches 20; Indels 57
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δ	1453 GAAGAGGAGCACATGGGGCAAGACCCTCACTCATCGAGAGCCAGCATCATCATCACCTGCTG 1512
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문	1744 CTGAGACCAAAACTGCAAAACATCCCCAGATCACCACAGCCATCATCATCAGCATCCCCACTCCC 1803
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망	1804 CCAGCGCTAACCCCAGAGGGGGAAAGTCGGCCACCCCCTGCCAGCCCCAGGCCCCAACACG 1863
Ş.	1993 AACATTCCTTCCATAACCAGCAATGTTGTCAAGGTCTCTGTCTTGTAAAAATCCCGCGGC 2052
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Search completed: April 6, 2005, 00:35:29 Job time : 11022.4 secs

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

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## Sequence 1, Application US/09178109 ; Sequence 1, Application US/09178109 ; Patent No. 6395477 ; GENERAL INFORMATION: ; APPLICANT: Cockett, Mark I. APPLICANT: Dilks, Daniel W. APPLICANT: Chang Ling, Huai-Ping ; APPLICANT: Sokol, Patricia T. TITLE OF INVENTION: Human Potassium Channel Polynucleotides and ; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and ; TITLE REFERENCE: ahp-98089 ; CURRENT APPLICATION NUMBER: US/09/178,109 ; CURRENT FILING DATE: 1998-10-23 ; NUMBER OF SEQ ID NOS: 4 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 1 ; LENGTH: 2121 TYPE: DNA ; ORGANISM: human US-09-178-109-1 US-09-178-109-1 Query Match Best Local Similarity Matches 2121; Conservative 121 ATCGGGTGGATGCCGGTGGCCAACTGCCCCATGCCCCTGGCCCGGCCGACAAGAACAAG 61 61 GATTTGCTGAACTAACTCCAAGCTGGTGTGCCTAGCGTCCGCGCGGGCGCCGAGA GCTGGAGTCACCATGGCGGCCGGAGTTGCCGCCCTGCCTTTTGCCCCGGGCTGCGGCC 100.0%; Score 2121; 100.0%; Pred. No. 0; tive 0; Mismatches DВ <u>,</u> ω •• Length Indels 2121; 0; Gaps

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RESULT 2
US-09-178-109-3
Sequence 3, Application US/09178109
Patent No. 6395477
GENERAL INFORMATION:
APPLICANT: Cockett, Mark I.
APPLICANT: Chang Ling, Huai-Ping
APPLICANT: Chang Ling, Huai-Ping
APPLICANT: Chang Ling, Huai-Ping
APPLICANT: Sokol, Patricia T.
TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
TITLE OF INVENTION: Polypeptides and Uses Therefor
FILE REFERENCS: ahp-98089
CURRENT APPLICATION NUMBER: US/09/178,109
CURRENT FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 2064
TYPE: DNA
ORGANISM: human
US-09-178-109-3
Query Match
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2064; Conservative 0; Mismatches 0; Indels 57; G
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081 ACTGTGATGTTTTATGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCCTGCC	- Q	

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Sequence 3, Application US/09142791A; Patent No. 6368823; GENERAL INFORMATION:
APPLICANT: Antoine Michel Alain Bril
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Faivre
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rouanet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH.30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT APPLICATION NUMBER: PCT/EP98/01901
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR APPLICATION NUMBER: US 9706377.0
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2072
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Best Local Similarity
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                                                    ATGGAGAGTTCAATGCAGAACTACCCATCCACAAGAAGTCCCTCACTGTCCAGCCACCCA
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APPLICANT: Antoine Michel Alain Bril
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Faivre
APPLICANT: Jean-Luc Javre
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rouanet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: UX 9706377.0
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
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## Sequence 957, Application US/09949016

## Patent No. 6812339

## GENERAL INFORMATION:

## APPLICANT: VENTER, J. Craig et al.

## TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

## FILE REFERENCE: CL001307

## CURRENT APPLICATION NUMBER: US/09/949,016

## CURRENT FILING DATE: 2000-04-14

## PRIOR APPLICATION NUMBER: 60/241,755

## PRIOR APPLICATION NUMBER: 60/237,768

## PRIOR APPLICATION NUMBER: 60/237,768

## PRIOR APPLICATION NUMBER: 60/231,498

## PRIOR FILING DATE: 2000-10-03

## PRIOR APPLICATION NUMBER: 60/231,498

## PRIOR FILING DATE: 2000-09-08

## NUMBER OF SEQ ID NOS: 207012

## SOFTWARE: FastSEQ for Windows Version 4.0

** SEQ ID NO 957

** LENGTH: 5333

** TYPE: NUMBER: 5333
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; ORGANISM: Human
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Best Local Similarity
Matches 1349; Conserv
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APPLICANT: Rutter, AAPPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761el Human Potassium Cha
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 3424
TYPE: DNA
ORGANISM: H. Bapiens
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Patent No. 6399761
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (257)...(2195)
OTHER INFORMATION: K+Hnov12
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                 TGGCCTTCTACGGCATCCTCCCGGAGATCATCGGGGGACTGCTGCTACGAGGAGTACAAGG
                                                                                    ACACCAAGGAGTACTTCTTCGACCGGGACCCCGAGGTGTTTCCGCTGCGTGCTCAACTTCT
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 TGGCTTTCTACGGCCTGGTTCCCGAGCTAGTCGGTGACTGCTTGCCTTGAAGAGTATCGGG
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Sequence 2456, Application US/09949016

; Sequence 2456, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER

FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

pRIOR APPLICATION NUMBER: 60/241,755

pRIOR FILING DATE: 2000-10-20

pRIOR APPLICATION NUMBER: 60/237,768

pRIOR FILING DATE: 2000-10-03

pRIOR FILING DATE: 2000-10-03

pRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; ELENGTH: 3260

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; ORGANISM: Human
US-09-949-016-2456
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US-09-949-016-2456
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Best Local Similarity
Matches 488; Conserv
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                       GACCACCTCACTCATCGAGAGCCCAGCATCATCACCTGCTGCACTGCCTGGAAAAAAACCAC
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AGGTAGTATACAAGAACTCAGCACGATTCAGATCAGATGTGTGGAGAACACCTCTGTC
                                                                                         CTCCCGTCGTAGTAAGAAGACCACCACACCTGCCCAATTCTAACCTGCCAGCTACTCGCCT
                                                                                                                                                        CTACCCATCCACAAGAAGTCCCTCACTGTCCAGGCCACCCAGGCCTCACTACCACCTGCTG
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nilarity 61.5%;
Conservative
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Pred. No. 8.3e-47;
D; Mismatches 245; Indels 6
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2293
LENGTH: 3004
TYPE: DNA
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US-09-949-016-2293
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US-09-949-016-2293
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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Best Local Similarity 53.4%;
Matches 712; Conservative
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 TACGGCATCCTCCCGGAGATCATCGGGGGACTGCTGCTACGAGGAGTACAAGGACCGCAAG
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                                                                                             AAGC --- TGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGACGAGCTGGCCTTC
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                                                           GGCCGCATCCGCCGGCCGGTCAACGTGCCCATCGACATTTTCTCCGAGGAGATCCGCTTC
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US-09-949-016-12066
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Sequence 12066, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
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; ORGANISM: Human
US-09-949-016-12066
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PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PastSEQ for Windows Version 4.
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Best Local Similarity 53.4%;
Matches 712; Conservative
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LENGTH: 7055
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TTCACCGTGGAGTACCTCCTGCGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCATCCGC 840
                                                     GCAGGAGCCTCCAGCTTCTCCGATCCCTTCTTCGTGGTGGAGACGCTGTGCATCATCTGG
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Pred. No. 3.4e-42;
0; Mismatches 575; Indels
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GENERAL INCORMATION:

GENERAL INCORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14035

LENGTH: 7056
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US-09-949-016-14035
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                                                                                            Query Match
Best Local Similarity
Matches 712; Conserv
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                                                                                                                                                                           ORGANISM: Human
                                                                                                                                                                                                              TYPE: DNA
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GCCGGAGTTGCGGCCTGGCCTTTTGCCCCGGGCTGCGGCCATCGGGTGGATGCCGGTG 138
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                                                                                                       Conservative
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                                                                                                    Score 240; DB 4; Length 7056; Pred. No. 3.4e-42; O; Mismatches 575; Indels 4
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AGCAAGTTCACAAGCATCCCTGCCTCGTTTTGGTACACCATTGTCACCATGACCACACTG
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 324

LENGTH: 3004
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US-09-949-016-324
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; ORGANISM: Human
US-09-949-016-324
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Best Local Similarity
Matches 710; Conserv
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Patent No. 681233
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                                                    GGCCGCATCCGCCGGCCGGTCAACGTGCCCATCGACATTTTCTCCGAGGAGATCCGCTTC
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Pred. No. 1.3e-41;
0; Mismatches 577;
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RESULT 13

US-09-949-016-1604

; Sequence 1604, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION

; FILE REFERENCE: CL001307
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.
SEQ ID NO 1604
LENGTH: 1802
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Pred. No. 3.6e-37;
0; Mismatches 445;
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TELEPHONE: 201-94-1744
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
FRIGTH: 2483 BASE PAIRS
                                                                                                                           Query Match 10.:
Best Local Similarity 53.:
Matches 565; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: June 5,1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08449
FILING DATE: 28 JUL 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4
FILING DATE:
                                                                                                                                                                                                                       TYPE: NUCLEIC ACID
STRANDEDNESS: SINGI
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
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TITLE OF INVENTION: Hun
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: 3.5 INC.
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: MS
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ADDRESSEE: CECCHI, STEWART
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
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                 GCTCAACTTCTACCGCACGGGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTA
                                                      CTACGACCCCGGCAAGCCCGAGTTCTACTTTGACAGGGACCCCGGACGCCTTCAAGTGTGT
                                                                                          CTTCAACGAGGACACCAAGGAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGT
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                                                                                                                           Score 216; DB 1; Length 2483; Pred. No. 3.9e-37; O; Mismatches 445; Indels 4
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& OLSTEIN
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RESULT 15
PCT-US94-08449A-3
; Sequence 3, Application PC/TUS9408449A
; GENERAL INFORMATION:
APPLICANT: LI, ET AL.
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2483 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Potassium Channel Protein 1 and NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PS/2
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SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UZIP: 07068
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                    CCCGGGCAGCAAGGAGCTGCCGTGCGGGGAGCGCTACTCGGTGGCCTTCTTCTGCCTGGA 761
                                                                                             CTTCTTCATCGCTGTCTCGGTCATCACCAACGTGGTGGAGACGGTGCCGTGCGGCACGGT
                                                                                                                                            GAAGTTCCTGGAGAAGCCCGAGTCGTCGTGCCCGGCGCGCGTGGTGGCCGAGCTCTCCTT
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Pred. No. 3.9e-37;
O; Mismatches 445;
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## RESULT 1 ABN84400 ID ABN8 WPI; 2002-556093/59. P-PSDB; ABB79584. Kv4.3; potassium channel; human; Alzheimer's disease; heart disease; nootropic; neuroprotective; cardiant; gene therapy; gene; ss. ABN84400; ABN84400 standard; cDNA; 2121 Cockett MI, 23-OCT-1998; 23-OCT-1998; 28-MAY-2002. Homo sapiens. Human Kv4.3 potassium channel (long form) cDNA. 01-OCT-2002 (first entry) US6395477-B1. (AMHP ) AMERICAN HOME PROD CORP Dilks DW, 98US-00178109. 98US-00178109 /\*tag= Location/Qualifiers /\*tag= a /product= "Kv4.3" Ling HC, B₽. Sokol PT;

The present sequence is that of cDNA encoding the long isoform of novel

Claim 5; Col 15-18; 19pp; English.

New isolated polynucleotide encoding human Kv4.3 potassium channel polypeptide, useful as probe in a diagnostic method for detecting acid encoding human Kv4.3, and for treating Alzheimer's and heart

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cc human potassium channel Kv4.3. To obtain the cDNA, oligonucleotides based cc on the published rat sequence were used to screen a whole heart cDNA library. A 511 bp fragment was obtained and used as a probe to rescreen cc the library. The resulting clones lacked the extreme 5' and 3' coding cregions, and 5' and 3' RACE was therefore used to amplify these sequences from a human brainstem cDNA library. 2 Isoforms of human Kv4.3 were cc identified. One form is full-length (hKv4.3 long) while the second form cc has a deletion of 19 amino acids in the carboxy domain after the predicted sixth transmembrane domain (hKv4.3 short). Human heart cc primarily expresses hKv4.3 long, whereas human brain contains both forms. CC The invention provides Kv4.3 polypeptides, polynucleotides, and methods cf invention provides Kv4.3 polypeptides, and methods collinated these polynucleotides. The kv4.3 polypeptides and cc polynucleotides are useful in the diagnosis, treatment and screening of human diseases relating to an excess or deficiency of hKv4.3 activity, including Alzheimer's disease and heart disease
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        The present sequence is that of cDNA encoding the short isoform of novel human potassium channel Kv4.3. 2 Isoforms of human Kv4.3 have been identified. One form is full-length (hKv4.3 long) while the second form has a deletion of 19 amino acids in the carboxy domain after the predicted sixth transmembrane domain (hKv4.3 short). Human heart primarily expresses hKv4.3 long, whereas human brain contains both forms. To obtain the present hKv4.3 short cDNA, PCR amplification was performed using primers that flanked the 57 bp insert in hKv4.3 long. The invention provides Kv4.3 polypeptides, polynucleotides, and methods for producing these polynucleotides. The Kv4.3 polypeptides and polynucleotides are
                                                                                                                                                                                                                                                                      New isolated polynucleotide encoding human Kv4.3 potassium channel polypeptide, useful as probe in a diagnostic method for detecting acid encoding human Kv4.3, and for treating Alzheimer's and heart
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09-DEC-1997;
11-DEC-1997;
                                                    This cDNA sequence codes for human Kv potassium channel hKv4.3 (see AAW79590). It shows about 92% identity in 1932 nucleotides to rat Kv4.3. A 1914 bp fragment corresponding to hhKv4.3 full-length cDNA was isolated from human heart cDNA by PCR amplification (see AAV61574-77). Another claimed polynucleotide (see AAV61571) encodes an isoform (see AAW79589) of hKv4.3 having 19 fewer amino acid residues. The invention relates to these hKv4.3 polynucleotides and polypeptides and to methods for producing such polypeptides by recombinant techniques. Also claimed are methods for utilising the hKv4.3 polynucleotides for the treatment of subjects in need of enhanced or reduced activity or expression of hKv4.3 polypeptide. These include the treatment of cardiac arrhythmias and Alzheimer's disease. The invention can also be used to identify agonists and antagonists of hKv4.3, and to detect disease associated with inappropriate hKv4.3 expression or activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arrhythmias and Alzheimer's disease.
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CTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACCACGCTGGAGCGCCCCCTGIIIIIIIIII		ATCGGGGACTGCTGCTACGAGGAGTACAAGGACCGCAA	
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CTGATTGTCCTCAACGTGAGTGGCGGAGGTTCCAGACCTGGAGGACCACGCTGGAGCGCCTGGATTGTCCTCAACGTGAGTGGCGGAGGTTCCAGACCTGGAGGACCACGCTGGAGCGCCTGATTGTCCTCAACGTGAGTGGCGCGCGAGGAGGTTCCTCTGAACGAGGACCACGAGGACCAACGAGTTGTCCTAACGACGACGAGGACCAACGAGGACCCCAAGTIIIIIIIIII		ACCATGTGGCGGGCCTTCGAGAACCCCCACACCAGCAC 	
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CTGATTGTCCTCAACGTGACTGGGCGGACGTTCCAGACCTTGGAGGACCACGCTGGAGGCCTTGATTGTCCTCAACGTGACTTGGACGGAGGTTCCAGACCTTGGAGGACCACGCTGGAGGCCTTGATTGTCCTCAACGTGACTTGGAGGAGGTTCCTTCTTCAACGAGGACACCAAGCTTGATTGTCCAACGTGACCACGTTGGAGGACACCAAGCTTGATTGTCCTTCAACGAACG		GCTCCCAGCCGCTACCGCTTCATCCGCAGCGTCATGAG	
CTGATTGTCCTCAACGTGAGTTGGGCGGAGGTTCCAGACCTGGAGGACCACGCTGGAGCGCTGGAGCGCTGGAGCGCTGGAGCGCTGGAGCGCTGGAGCGCTGGAGCGCTGGAGCGCTGGAGCGCTTGAACGTTGCACCACGCTGGAGCGCGCTTGAACGTGGACCACGCTGGAGCGCCTTGAACGTGGACCACGCTTGGACCGCCTTGAACGAGACCACGCTTGAACCACGCTTGAACCACGCTTGAACCACGCTTGAACCACGCTTGAACCAAGGACACCAAGGACACCCAAGGACACCCCAAGGACCCCCAAGGACCCCCAAGGACCCCCAAGGACCCCCAAGGACCCCCAAGGACCCCCAAGGACCCCCAAGGACCCCCAAGGACCCCCAAGGACCCCCAAGGACCCCCAAGGACCCCCAACGTTCTTCTACCAACTTCTACCCACCAAGGACCACCACGACGACCACGACGACCACCAC		ATGCCCTACTACATCGGTCTGGTCATGACCAACAACGA 	
CTGATTGTCCTCAACGTGAGTGGGGGGAGGTTCCAGACCTTGGAGGACCACGCTGGAGGCCTGGAGGACCACGCTGGAGGACCACGCTGGAGGACCACGCTGGAGGACCACGCTGGAGGACCACGCTGGAGGACCACGCTGGAGGACCACGCTGGAGGACCACGCTGGAGGACCACGCTGGAGGACCACGCTGGAGGACCACGCTGGAGGACCACGCTGGAGGACCACGCTGGAGGACCACGAGGACACCAAGGATTCTTCTTCTAACGAGGACCACCAAGGACTACCAAGGACTACCAAGGACCACCAAGGACACCCAAGGACACCCAAGGACACCCAAGGACACCCAAGGACACCCAAGGACACCCAAGGACACCCAAGGACACCCAAGGACACCCAAGGACACCCAAGGACACCCAAGGACACCCAAGGACACCCAAGGACACCCAAGGACACCCAAGGACACCCAAGGACACCCAAGGACACCCAAGGACCACC		ACGCTCCGGGTCTTCCGCGTCTTCAGGATCTTCAAGTT	
TRAITIGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTTGGAGGACCACGCTTGGAGGGCCTTGAITIGITIGITIGITIGITIGITIGITIGITIGITIG		CGGATCCTGGGCTACACACTGAAGAGCTGTGCCTCCGA	
CTGATTGTCTCAACGTGAAGTGGGGGAGGTTCCAGACCTGGAAGCACCACGTGGAGGCC  TACCCGGACACCCTTCGTGGGCAGGACGACGAGGAGAACCACGCTGGAGGCC  TACCCGGACACCCTTCTGGGCAGCACGGAGAAGAAGAAGAAGAACCACGAGACCCAAG  TACCCGGACACCCTTCTGGGCAGCACGGAGAAAGAAGTTCTTCTCAACGAGACACCCAAG  TACCCGGACACCCTTCTGGGCAGCACGAGAGAGAAGAAGTTCTTCTCAACGAACACCAAG  TACCCGGACACCCTTCTGGACCGGGACACGAGAGAGAGATTCTTCTCCAACGACGACCACCAAG  AGGTACTTCTTCGACCGGGCTACGAGTGCATCCTCCGCTGCTCAACCTCCAACCTTCTACCGCACG  GGGAAGCTTCCTTCCAACCACGAGACCCCGAAGTTCCTTCC		CTCACCATGGCCATCATCATCTTTGCCACTGTGATGTT 	
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ADF91397 standard; CDNA; 1968 BP.

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Wild-type hKv4.3 CDNA #SEQ IJ

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Antiarrhythmic; cardiovascular; anticonvulsant; cerebroprotective; tranquiliser; sedative; neuroprotective; notropic; antiparkinsonian; nematode worm; voltage-gated potassium channel; Kv4; agonist; antagonist; blocker; pharmaceutical; agrochemical; veterinary; arrhythmia;

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                                                                                                                                                                                                                                                                                                                        The invention relates to a nematode worm that expresses a heterologous nucleotide sequence encoding a functional voltage-gated potassium channel of the Kv4 family, or its analog, mutant, variant, homolog, ortholog, part or fragment. The nematode worm is useful in determining whether a compound interacts with the voltage-gated potassium channel of the Kv4 family or whether a compound is an agonist, antagonist, opener and/or blocker of the voltage-gated potassium channel expressed by the nematode worm. The methods are used for identifying and developing compounds that cinteract with voltage-gated potassium channels of the Kv4 family. The compounds may be used in the development and/or preparation of compositions for pharmaceutical, agrochemical and/or veterinary use. These may be used in preparing compositions for preventing or treating diseases or conditions such as arrhythmia, tachycardia, congestive heart failure, epilepsy, stroke, traumatic brain injury, anxiety, insomnia, carrescents will-type have a conditions of sisease. The current sequence
                                                                                                                                                                                                                            Query Match
Best Local Sim:
Matches 1963;
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P-PSDB;
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15-MAY-2002; 2002US-0378076P
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                                                                                                                                                                                                                                                                                                                represents wild-type hKv4.3 cDNA.
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                 TACCCGGACACCCTGCTGGGCAGCACGGAGAAGGAGTTCTTCTTCAACGAGGACACCCAAG
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                            GCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAACAGGCAGTTCGAATGCA
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                                                                                     GTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAGAGCTGATAAACGCAGG
                                                                                                                                                AAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCATTGCCCCTGCCAGTCCCT
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             GCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAACAGGCAGTTCGAATGCA
                                                                     GTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAGAGCTGATAAACGCAGG
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27-MAR-1997;
09-DEC-1997;
11-DEC-1997;
                                                                                                                                                                                                                      Human Kv potassium channel hKv4.3 (shorter isoform) cDNA.
                                                                                                                                                                                                                                              11-JAN-1999
                                                                                                                                                                                                                                                                   AAV61571;
                                                                                                                                                                                                                                                                                        AAV61571 standard; cDNA; 2104
                                                                                                                                                                                   therapy; diagnosis;
                                              23-MAR-1998;
                                                                    01-OCT-1998
                                                                                          WO9842833-A2
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97GB-00006377.
97EP-00402971.
97EP-00403007.
                                              98WO-EP001901.
                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                            entry)
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                                                                                                                                                                                               hKv4.3; human;
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This cDNA sequence codes for human Kv potassium channel hKv4.3 (see AAW79589). It shows about 92% identity in 1913 nucleotides to rat Kv4.3. A 1914 bp fragment corresponding to hKv4.3 full-length cDNA was isolated from human heart cDNA by PCR amplification (see AAV61574-77). Another claimed polynucleotide (see AAV61572) encodes an isoform (see AAW79590) of hKv4.3 having an additional 19 amino acids. The invention relates to these hKv4.3 polynucleotides and polypeptides and to methods for producing such polypeptides by recombinant techniques. Also claimed are methods for utilising the hKv4.3 polynucleotides for the treatment of subjects in need of enhanced or reduced activity or expression of hKv4.3 polypeptide. These include the treatment of cardiac arrhythmias and Alzheimer's disease. The invention can also be used to identify agonists and antagonists of hKv4.3 and to detect disease associated with inappropriate hKv4.3 expression or activity
                                                                                                                                                                                                                                                                                                                                                                                                                      New potassium channel polypeptides, hKv4.3 poly:nucleotide(s) useful in the treatment arrhythmias and Alzheimer's disease.
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    and hKv4.3-encoding
of disorders including cardiac

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Query Match Best Local Similarity Matches 1914; Conserva Sequence 2104 BP; 461 A; 678 C; 559 G; 406 T; 0 U; 0 Other; 86.7%; ; Score 1838; DI ; Pred. No. 0; 0; Mismatches BG 2; Length 2104;

Matches	Matches 1914; Conservative 0; Mismatches 15; Indels 57; Gaps 1;
Q	73 ATGGCGGCCGGAGTTGCGGCCTGGCCTGTTTGCCCGGGCTGCGCCATCGGGTGGATG 132
מם	1 ATGCCGCAGGAGTTGCAGCCTGGCCTGTTTGCCCCGGGCTGCGGCCATCGGGTGGATG 60
8	133 CCGGTGGCCAACTGCCCCATGCCCCTGGCCCCGGCCACAACAACAAGCGGCAGGATGAG 192
Дb	61 CCGGTGGCCAACTGCCCCATGCCCCTGGCCCCGGCCGACAAGAACAAGCGGCAGGATGAG 120
γQ	193 CTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACCACGCTGGAGCGC 252
Db	121 CTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACCACGCTGGAGCGC 180
Ş	253 TACCCGGACACCCTGCTGGGCAGCACGGAGAAGGAGTTCTTCTTCAACGAGGACACCAAG 312
Вb	181 TACCCGGACACCCTGCTGGGCAGCACGAGAAGGAGTTCTTCTTCAACGAGGACACCAAG 240
γQ	313 GAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTTCTACCGCACG 372
Db	241 GAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTTCTACCGCACG 300
γ	373 GGGAAGCTGCACTACCGCGCTACGAGTGCATCTCTGCCTACGACGACGAGCTGGCCTTC 432
Db	301 GGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGACGACGAGCTGGCCTTC 360
γ2	433 TACGGCATCCTCCCGGAGATCATCGGGGACTGCTGCTACGAGGAGTACAAGGACCGCAAG 492
Дb	361 TACGGCATCCTCCCGGAGATCATCGGGGACTGCTGCTACGAGGAGTACAAGGACCGCAAG 420
γ	493 AGGGAGAACGCCGAGCGGCTCATGGACGACGACGACTCGGAGAACAACCAGGAGTCCATG 552
В	421 AGGGAGAACGCCGAGCGGCTCATGGACGACAACGACTCGGAGAACCAACC
Qγ	553 CCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGCCCTTCGAGAACCCCCACACCACCAGCACG 612
Db	481 CCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGCCTTCGAGAAACCCCCACACCAGCACG 540
γQ	613 CTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTCGGTCATCACCAAC 672
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This cDNA sequence codes for human Kv potassium channel hKv4.3 (see AAW79591). It was isolated using expressed sequence tag analysis. The sequence has about 91% identity in 1914 nucleotide residues with rat Kv4.3 potassium channel. Full-length hKv4.3 cDNA clones (see AAV61571-72) are also claimed. The invention relates to hKv4.3 polynucleotides and

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09-DEC-1997;
11-DEC-1997;
                                                                   New potassium channel polypeptides, hKv4.3 poly:nucleotide(s) useful in the treatment arrhythmias and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                      Human
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                                                    Claim
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DB; AAW79591.
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diagnosis; ss.
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                                                                                                                 ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
                                                                                                                                   Human
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2000US-00561778.
2000US-00640173.
2000US-00656668.
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Best Local Similarity
Matches 1349; Conserv
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New polynucleotides encoding tumor proteins, treating or inhibiting the development of cancer, particularly ovarian cancer, and for stimulating and/or expanding T cells specific for a tumor protein.
                                                                                                                                                                                                                                                                                                                                                                                           14-NOV-2000; 2000US-00713550.
03-APR-2001; 2001US-00825294.
02-OCT-2001; 2001US-00970966.
02-AUG-2002; 2002US-00212677.
Example 12; SEQ ID NO 253; 221pp; English.
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to detecting the presence of an ovarian cancer in a patient by stimulating and/or expanding T cells specific for the tumour protein. products of the invention can also be used in a method to inhibit the development of a cancer in a patient comprising (a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one ovarian tumour protein, such that T cell proliferate and (b) administering to patient the proliferated T cells. The cytostatic polynucleotides or polypeptides described in the invention are useful for treating or inhibiting the development of cancer, particularly ovarian cancer and stimulating and/or expanding T cells specific for a tumour protein or Sequence gene therapy. This invention describes a novel ovarian tumour protein which to detecting the presence of an ovarian cancer in a patient by 2351 B₽; 572 A; 606 ü 591 G; 582 T; 0 U; 0 Other; can be used for The the

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                                                                                                                                             GCTGGCCTTCTACGGCATCCTCCCGGAGATCATCGGGGACTGCTGCTGCTACGAGGAGTACAA
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                                                                     GGACCGCAAGAGGGAGAACGCCGAGCGGCTCATGGACGACAACGACTCGGAGAACAACCA
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D; Mismatches 491;
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This invention relates to novel isolated polynucleotides and methods fithe therapy and diagnosis of cancer, particularly ovarian cancer. Specifically, it refers to these polynucleotides and the encoded polypeptides thereof, as well as immunogenic peptides, antibodies, antigen presenting cells (APCs) and immune system cells (e.g. T cells) that are targeted to those cells expressing the proteins of interest. The present invention describes methods that are useful for stimulating and or expanding T cells specific for a tumourigenic protein (i.e. T cells)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2351 BP; 572 A; 606 C; 591 G; 582 T; 0 U; 0 Other;
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                                                              New polynucleotides encoding tumor proteins, treating development of cancer, particularly ovarian cancer, ar and/or expanding T cells specific for a tumor protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to detecting the presence of an ovarian cancer in a patient by stimulating and/or expanding T cells specific for the tumour protein. products of the invention can also be used in a method to inhibit the development of a cancer in a patient comprising (a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one ovarian tumour protein, such that T cell proliferate and (b) administering to patient the proliferated T cells. The cytostatic polynucleotides or polypeptides described in the invention are useful for treating or inhibiting the development of cancer, particularly ovarian cancer and stimulating and/or expanding T cells specific for a tumour protein or
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15-AUG-2000;
07-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel ovarian tumour protein which can be u to detecting the presence of an ovarian cancer in a patient by stimulating and/or expanding T cells specific for the tumour protein. products of the invention can also be used in a method to inhibit the development of a cancer in a patient comprising (a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one ovarian tumour protein, such that T cell proliferate and (b) administering to patient the proliferated T cells. The cytostatic polynucleotides or polypeptides described in the invention are useful for treating or inhibiting the development of cancer, particularly ovarian cancer and stimulating and/or expanding T cells specific for a tumour protein or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding tumor proteins, treating or inhibiting the development of cancer, particularly ovarian cancer, and for stimulating and/or expanding T cells specific for a tumor protein.
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03-APR-2001; 2001US-00825294.
02-OCT-2001; 2001US-00970966.
02-AUG-2002; 2002US-00212677.
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15-AUG-2000;
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DT 15-APR-2004 (first entry)
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DT 15-APR-2004 (first entry)
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AC ADJ11253;
XX
Human ovarian tumour antigen DNA SeqID 254.
XX
CE Human ovarian cancer; immunogenic; antibody;
XX
CE ART APR 15-APR 15-APR 2003; 2003US-00365178.
CE ART 10-SEP-1999; 99US-00394374.
CE ART 10-SEP-1999; 99US-0
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02-OCT-2001;
02-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to novel isolated polynucleotides and methods for the therapy and diagnosis of cancer, particularly ovarian cancer. Specifically, it refers to these polynucleotides and the encoded polypeptides thereof, as well as immunogenic peptides, antibodies, antigen presenting cells (APCs) and immune system cells (e.g. T cells) that are targeted to those cells expressing the proteins of interest. The present invention describes methods that are useful for stimulating and/ or expanding T cells specific for a tumourigenic protein (i.e. T cell therapy). Furthermore, compositions can be used for the diagnosis, treatment and/ or prevention of ovarian cancer by stimulating an immune response in a patient. Accordingly, these compositions exhibit cytostatic activity. This polynucleotide is a human ovarian tumour antigen DNA sequence given in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated ovarian polypeptide, useful as in a patient.
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GGAGAGCGCCTTGCCCACCATGACTGCAAGGCAGAGGGTCTGGAGGGCCTTCGAGAACCC
                                                           GGATCGCAGGCGAGAGAACGCCGAGCGCCTGCAGGACGCGCGATACCGACACCGCTGG
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Other;

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03-APR-2001;
02-OCT-2001;
02-AUG-2002;
05-FEB-2003;
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01-MAY-2000;
15-AUG-2000;
07-SEP-2000;
This invention relates to novel isolated polynucleotides and methods for the therapy and diagnosis of cancer, particularly ovarian cancer. Specifically, it refers to these polynucleotides and the encoded polypeptides thereof, as well as immunogenic peptides, antibodies, antigen presenting cells (APCs) and immune system cells (e.g. T cells) that are targeted to those cells expressing the proteins of interest. present invention describes methods that are useful for stimulating any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; ds; ovarian antigen presenting cytostatic; gene.
                                                                                                                                                                                                                      polypeptide,
in a patient.
                                                                                                                                                                                                                                       Novel isolated ovarian tumor polynucleotide encoding ovarian tumor polypeptide, useful as probes of primers for detecting presence of
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; 2000US-00640173.
; 2000US-00656668.
; 2000US-00713550.
; 2001US-00825294.
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; 2002US-00212677.
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                       CAGCATCCCCACTCCCCCAGCCCTAACCCCAGAGGGGGAAAGTCGGCCA 1965
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01-MAY-2000; 2000US-00561778.
15-AUG-2000; 2000US-00640173.
07-SEP-2000; 2000US-0065668.
14-NOV-2000; 2000US-00713550.
03-APR-2001; 2001US-00825294.
02-OCT-2001; 2001US-00970966.
                                                                                                                                                                                                                                                                                                                                                      Sequence 5333
                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated polynucleotide. The invention is used to diagnose, prevent or treat cancer, particularly ovarian cancer.

The present sequence represents a human ovarian carcinoma cDNA homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide encoding an ovarian tumor protein for diagnosing, preventing or treating cancer, particularly ovarian
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P-PSDB; ADM43518.
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                                                                               AGAAACTCAGCAGTATTTCTTTGACCGTGACCCAGACATCTTCCGCCACATCCTGAATTT
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<b>1</b> 6	1497 GCATCATCACCTGCTGCACTGCCTGGAAAAAACCACTGGGTTGTCCTATCTTGTGGATGA 155
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<b>ω</b> σ	1377 AGGCAGTTCGAATGCATACCTGCACAGCAAGCGCAACGGGCTCCTCAACGAGGCGCTGGA 1430
<b>&amp;</b> 6	1317 AGCTGATAAACGCAGGGCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAAC 137/
ω σ	1257 TGCCCTGCCAGTCCCTGTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAG 1310
<b>ω</b> σ	1197 TAAGACGATTGCAGGGAAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCAT 125
<b>a</b> o	1137 TGCCTCGTTTTGGTACACCATTGTCACCATGACCACACTGGGATACGGAGACATGGTGCC 119
<b>ω</b> σν	1077 TGCCACTGTGATGTTTTATGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCC 1130
<b></b>	1017 GAGCTGTGCCTCCGAACTGGGCTTTCTTCTTCTCTCCCTCACCATGGCCATCATCATCTT 107/
& <b>6</b>	957 CAGGATCTTCAAGTTTTCCCGCCACTCCCAGGGCCTGCGGATCCTGGGCTACACACTGAA 101
80	897 CATGACCAACAACGAGGACGTGTCCGGCGCCTTCGTCACGCTCCGGGGTCTTCCGCGTCTT 956
œ	837 CCGCAGCGTCATGAGCATCATCGACGTGGTGGCCATCATGCCCTACTACATCGGTCTGGT 896
89	777 GATCTTCACCGTGGAGTACCTCCTGCGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCAT 836
œ	717 GCTGCCGTGCGGGAGAGCGCTACTCGGTGGCCTTCTTCTGCCTGGACACGGCGTGCGT
œ	660 GGTCATCACCAACGTGGAGACGGTGCCGTGCCGGCACGGTCCCGGGCAGCAAGGA 716
80	600 CCACACCAGCACGCTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTC 659
α	543 GGAGTCCATGCCCTCGCCTCAGCTTCCGCCAGACCATGTGGCGGGCCCTTCGAGAACCC 599
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                                                                GATICCACATCCAGGGCAGTGAGCAGCCCTCCCTCACAACCAGTCGCTCCAGCCTTAATTT 1856
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1: /cgn2 6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2-6/ptodata/1/pubpna/US06 NEW PUB.seq:*

3: /cgn2-6/ptodata/1/pubpna/US06 PUBCOMB.seq:*

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6: /cgn2-6/ptodata/1/pubpna/US08 NEW PUB.seq:*

7: /cgn2-6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

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Sequence 10, Appl Sequence 13, Appli Sequence 3, Appli Sequence 3, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 92, Appli Sequence 92, Appli	256 255 263 263 255 255 255 255 255 255 255 255 255 25	e 9, Ap e 373, e 255, e 255, e 255, e 24777

## ALIGNMENTS

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CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US/09/178,109
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 2121
TYPE: DNA
ORGANISM: human
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US-10-062-879-1
                                                                                                                                   Query Match 100.0%; Score 2121; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 4121; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10062879 Publication No. US20020127649A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cockett, Mark I.
APPLICANT: Dilks, Daniel W.
APPLICANT: Chang Ling, Huai-Ping
APPLICANT: Sokol, Patricia T.
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/062,879
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Human Potassium Channel Polynucleotides
TITLE OF INVENTION: Polypeptides and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: ahp-98089
GATTTGCTGAACTAACTCCAAGCTGGTGTGCCTAGCGTCCGCGGCGGCTGCCGAGGA
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1081 ACTGTGATGTTTTATGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCCTGCC 1140	21 TGTGCCTCCGAACTGGGCTTTCTTCTCTCTCCCTCACCATGGCCATCATCATCTTTGCC 108 	61 ATCTTCAAGTTTTCCCGCCACTCCAGGGCCTGCGGATCCTGGGCTACACACTGAAGAGC 10	01 ACCAACAACGAGGACGTGTCCGGCGCCTTCGTCACGCTCTCCGGGTCTTCAGG 9 	41 AGCGTCATGAGCATCATCGACGTGGTGGTGGCCATCATGCCCTACTACATCGGTCTGGTCATG 90	81 TTCACCGIGGAGIACCICCIGCGGCTCTTCGCGGCTCCCAGCCGCIACCGCTTCATCCGC 84	21 CCGTGCGGGGAGCGCTACTCGGTGGCCTTCTTCTGCCTGGACACGGCGTGCGT	61 GTCATCACCAACGTGGTGGAGACGGTGCCGTGCGGCACGGTCCCGGGCAGCAAGGAGCTG 72 	01 CACACCAGCACGCTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTCG 66 	41 CAGGAGTCCAIGCCCTCGCTCAGCTTCCGCCAGACCAIGIGGCGGGCCTTCGAGAACCCC 60 	81 AAGGACCGCAAGAGGGAGAACGCCGAGCGGCTCATGGACGACAACGACTCGGAGAACAAC 54 	21 GAGCTGGCCTTCTACGGCATCCTCCCGGAGATCATCGGGGACTGCTGCTACGAGGAGTAC 48 	61 TTCTACCGCACGGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGAC 42	01 GAGGACACCAAGGAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAAC 36 	241 ACGCTGGAGCGCTACCCGGACACCCCTGCTGGGCAGCACGGAGAAGGAGGTTCTTCTTCAAC 300	181 CGGCAGGATGAGCTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACC 240	61 GCTGGAGTCACCATGGCGGCCGAGTTGCGGCCTGGCCTTTTTGCCCGGGCTGCCCTGCCC 120  121 ATCGGGTGGATGCCGGTGGCCAACTGCCCCATGCCCCTGGCCCCGGCCGACAAGAACAAG 180
RESULT 2 US-10-062-879-3 ; Sequence 3, Application US/10062879 ; Publication NO. US20020127649A1 ; GENERAL INFORMATION: ; APPLICANT: Cockett, Mark I. ; APPLICANT: Dilks, Daniel W.	Qy 2101 AGTCGTATTAAAGCCGAATTC 2121	QY 2041 AAÁTCCCGCGGCCATGGCGGCCGGGAGCATGCGACGTCGGGCCCAATTCGCCCTATAGTG 2100	Qy 1981 GGCCCCAACACGAACATTCCTTCCATAACCAGCAATGTTGTCAAGGTCTCTGTCTTGTAA 2040	QY 1921 ATCCCCACTCCCCAGCGCTAACCCCAGAGGGGGAAAGTCGGCCACCCCCTGCCAGCCCA 1980	QY 1861 GCAGACGACGACCGAGACCAAAACTGCAAAACATCCCAGATCACCACAGCCATCATCAGC 1920	Qy 1801 CACATCCAGGGCAGTGAGCAGCCCTCACAAACCAGTCGCTCCAGCCTTAATTTGAAA 1860	QY 1741 CTGCCCAATTCTAACCTGCCAGCTACTCGCCTGCGCAGCATGCAAGAGCTCAGCACGATC 1800	Qy 1681 TCCAGCCACCCAGGCCTCACTACCACCTGCTGCTCCCGTCGTAGTAAGAAGACCACACAC 1740	بر بر	QY 1561 CTGTTATCTGTACGAACCTCCACCATCAAGAACCACGAGTTTATTGATGAGCAGATGTTT 1620	. Qy 1501 CATCACCTGCACTGCACTGCACTGGAAAAAAACCACTGGGTTGTCCTATCTTGTGGATGATCCC 1560	Y 1441 ACGGGCACCCCAGAAGAGGGAGCACATGGGCAAGACCACCTCACTCA	OY 1381 AGTTCGAATGCATACCTGCACAGGCAAGGGCGCAACGGGGCTCCTCAACGAGGCGCTGGAGCTG 1440	Db 1321 GATAAAAGGCAGGGCACAAAAAGAAAGGCCGCCTTGCCAGGATCCGTGTGGCCAAAAACAGGC 1380	Y 1261 CTGCCAGTCCCTGTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAGAGCT 13 b 1261 CTGCCAGTCCCTGTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAGAGCT 13	Y 1201 ACGATTGCAGGGAAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCATTGCC

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; APPLICANT: Chang Ling, Huai-Ping
; APPLICANT: Sokol, Patricia T.
TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; TITLE OF INVENTION: Polypeptides and Uses Therefor
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/10/062,879
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/178,109
; PRIOR APPLICATION NUMBER: US/09/178,109
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: human
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                                    CACACCAGCACGCTGGCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTCG
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Query Match  Best Local Similarity 70.7%; Pred. No. 2.6e-248;  Matches 1349; Conservative 0; Mismatches 491; Indels 69; Gaps 5;  Qy  66 AGTCACCATGGCGGCGGAGTTGCGGCTGGCTGCCTTTTGCCAGGCCATCGG 125	RESULT 4  US-10-361-811-253 ; Sequence 253, Application US/10361811 ; Publication No. US20030206918A1 ; GENERAL INFORMATION: APPLICANT: Fanger, Gary R. APPLICANT: Fling, Steven P. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.484C8 ; CURRENT APPLICATION NUMBER: US/10/361,811 ; CURRENT FILING DATE: 2003-02-05 ; NUMBER OF SEQ ID NOS: 293 ; SOFTWARE: FASTSEQ for Windows Version 4.0 ; SEQ ID NO 253 ; LENGTH: 2351 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-361-811-253	Oy  1557 TCCCCTGTTATCTGTACGAACCTCCACCAAGAACCACAGAGTTTATTGATGAGAT 1616  1896
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43 CGCTACAGTTATGTTCTACGCAGAGAAGGGGTCTTCGGCTAGCAAGTTCACCAGCATCCC 150  7 TGCCTCGTTTTTGGTACCCATTGCAGAGAAGGGGTCTTCGGCTAGCAAGTTCACCAGCATCCC 150  7 TGCCTCGTTTTTGGTACCCATTGCAGAGAAGGGGTCTTCGGCTAGCAAGTTCACCAGCATCGCC 119  8 TGCCAGCCTTCTGGTATACCATCGTCACCATGACAACACCAGGATATGGTAGCAATGGTGCC 156  97 TAAGACGATTGCAGGGAAGATCTTTCGGCTCCATCTGCTCCTTGAGGTAGTGGCTCCTGGTCAT 125  83 AAAAACCATAGCAGGGAAGATTTTTTGGTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAG 131  1	777 GATCTTCACCGTGGAGTACCTCCTGCGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCA	363 CTACCGCACGGGAAGCTGCACTACCCGCGCTTACGAGGAGTGCATCTCTGCCTACGACGACGA 422

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GENERAL INCOMPLETATION:

APPLICANT: Fainger, Gary R.

APPLICANT: Fling, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.484C9

CURRENT APPLICATION NUMBER: US/10/369,186

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 293

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 253

LENGTH: 2351

TYPE: DNA

ORGANISM: Homo sapiens
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US-10-369-186-253
; Sequence 253, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
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APPLICANT: Chenault, Ruth A.

APPLICANT: Fanger, Gary R.

APPLICANT: Harlocker, Susan L.

APPLICANT: McNeill, Patricia D.

ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

ITITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.484C7

CURRENT APPLICATION NUMBER: US/10/212,677

CURRENT FILING DATE: 2002-08-02

NUMBER OF SEQ ID NOS: 288

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 252

LENGTH: 5333

TYPE: DNA

ORGANISM: Homo sapiens

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                                                      Query Match
Best Local Similarity
Matches 1349; Conserv
                                                                                                                                                                                                                                                                                                                                                                                Sequence 252, Application US/10212677 Publication No. US20030129192A1 GENERAL INFORMATION:
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Pred. No. 3.2e-248;
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Sequence 254, Application US/10212677

Publication No. US20030129192A1

GENERAL INFORMATION:
APPLICANT: Chenault, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CAN
FITLE REFERENCE: 210121.484C7
CURRENT APPLICATION NUMBER: US/10/212,677
CURRENT APPLICATION UMBER: US/10/212,677
CURRENT FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 288
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 254
LENGTH: 5333
                                                                                                                                                                                                                                                                                                        RESULT 7
US-10-212-677-254
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                                                            CAGGATCTTCAAGTTTTCCCGCCACTCCCAGGGCCTGCGGATCCTGGGCTACACACTGAA 1016
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Sequence 252, Application US/10361811
Publication No. US20030206918A1
GENERAL INFORMATION:
APPLICANT: Fanger, Gary R.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
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CURRENT APPLICATION NUMBER: US/10/361, CURRENT FILING DATE: 2003-02-05
NUMBER OF SEQ ID NOS: 293
SOFTWARE: FastSEQ for Windows Version SEQ ID NO 252
LENGTH: 5333
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APPLICANT: Filing, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.484C8

CURRENT APPLICATION NUMBER: US/10/361,811

CURRENT FILING DATE: 2003-02-05

NUMBER OF SEQ ID NOS: 293

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 254

LENGTH: 5333

TYPE: DNA

ORGANISM: Homo sapiens

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Publication No. US20030206918A1
GENERAL INFORMATION:
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Best Local Similarity 70.7%;
Matches 1349; Conservative
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RESULT 10

US-10-369-186-252

Sequence 252, Application US/10369186

Publication No. US20030232056A1

GENERAL INFORMATION:

APPLICANT: Fanger, Gary R.

APPLICANT: Fling, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.484C9

CURRENT APPLICATION NUMBER: US/10/369,186

CURRENT APPLICATION NUMBER: US/10/369,186

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 293

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 252

LENGTH: 5333
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Pred. No. 3.2e-248;
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Best Local Similarity 70.7
Matches 1349; Conservative
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GENERAL INFORMATION:

APPLICANT: Fanger, Gary R.

APPLICANT: Fling, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.484C9

CURRENT APPLICATION NUMBER: US/10/369,186

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 293

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 254

LENGTH: 5333

TYPE: DNA

ORGANISM: Homo sapiens

US-10-369-186-254
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ACTGTCCAGCCACCCAGGCCTCACTACCACCTGCTGCTCCCGTCGTAGTAAGAAGACCAC
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                                                            CTTTGAAGAAAGCTGCATGGAAGTTGCAACTGTTAATCGTCCTTCAAGTCACAGTCCTTC
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Sequence 9, Application US/10121746

; Sequence 9, Application US/20030036648A1

; GENERAL INFORMATION:

APPLICANT: Miller, Andrew P.

APPLICANT: Miller, Mark Edward

APPLICANT: Hu, Ping

; APPLICANT: Rutter, Marc

APPLICANT: Wang, Jian-Wang

TITLE OF INVENTION: NO. US2003036648A1el Human Potassium

FILE REFERENCE: SEQ-15P

CURRENT APPLICATION NUMBER: US/10/121,746

CURRENT FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: US/09/336,643A

PRIOR FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: 1999-01-19

PRIOR APPLICATION DATE: EARLIER FILING DATE: 1999-01-19

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22

NUMBER OF SEQ ID NOS: 87

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 3424
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Best Local
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TYPE: DNA
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NAME/KEY: CDS
LOCATION: (257)...(2195)
OTHER INFORMATION: K+Hnov12
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          GCCCTGCCAGCAGGCAGCTCCCTGCGGCAGCAGCTCTGGCGGGCCTTCGAGAATCCACAC
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GENERAL INFORMATION:

APPLICANT: Hyseq Inc.

TITLE OF INVENTION: No. US20040053248A1el Nucleic Aci
FILE REFERENCE: 784PCT

CURRENT APPLICATION NUMBER: US/10/296,115

CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOMBER: US09/552,317
FRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 1478

SEQ ID NO 373

LENGTH: 2578
TYPE: DNA
ORGANISM: Homo sapiens
US-10-296-115-373
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Best Local Similarity 72.9%;
Matches 1075; Conservative
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CCTCGCT-----CAGCTTCCGCCAGACCATGTGGCGGCCTTCGAGAACCCCCAC
                                                                                                           AGGGAGAACGCCGAGCGGCTCATGGACGACAACGACTCGGAGAACAACCAGGAGTCCATG
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RESULT 14
US-10-212-677-255
; Sequence 255, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
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APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C7
CURRENT APPLICATION NUMBER: US/10/212,677
CURRENT FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 288
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 255
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Best Local Similarity
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CCGCAGCGTCATGAGCATCATCGACGTGGTGGCCATCATGCCCTACTACATCGGTCTGGT
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                                                              GATCTTCACCGTGGAGTACCTCCTGCGGGCTCTTCGCGGGCTCCCAGCCGCTACCGCTTCAT
                                                                                                                        GGTCATCACCAACGTGGTGGAGAACGGTGCCGTGCGGCACGGTCCCCGGG----CAGCAAGGA
                                                                                                                                                                                                                                        CCACACCAGCACGCTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTC
                                                                                                                                                                                                                                                                                                   GGAG---TCCATGCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGGCCTTCGAGAACCC
                                                                                                                                                                                                                                                                                                                                                               ACTGGCCTTCTTTGGCCTCATCCCGGAAATCATCGGCGACTGCTGTTATGAGGAGTACAA
                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGGCCTTCTACGGCATCCTCCCGGAGATCATCGGGGGACTGCTACCGAGGAGGACTACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTCACCATGGCGGAGTTGCGGCCTGGCCTTTTGCCCGGGCTGCGGCCATCGG
                                               GATCTTCACAGTTGAGTATTTGCTTCGCCTGGCTGCAGCGCCTAGTCGTTACCGTTTTGT
                                                                                                       ACTGCCCTGTGGAGAGCGGTATGCTGTGGCCTTCTTCTGCATGGACACGGCCTGCGTCAT
                                                                                                                                                             TGTCATCGCGAATGTGGTGGAAACAGTGCCGTGCGGATCAAGCCCCAGGTCACATTAAAGA
                                                                                                                                                                                                                         CCACACCAGCATGGCCCTGGTGTTCTACTATGTCACGGGGTTTTTCATTGCCGTCTC
                                                                                                                                                                                                                                                                                GGAGAGCGCCTTGCCCACCATGACTGCAAGGCAGAGGGTCTGGAGGGCCTTCGAGAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTACCGCACGGGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGACGA
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Pred. No. 3.1e-177;
0; Mismatches 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5404;
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Search completed: April 6, 2005, 05:57:51 Job time : 2204.94 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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             1839.2
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Match Length DB
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Gapop 10.0 , Gapext 1.0
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12979.627 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_est1: *
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                                      BZ203918
CNS02DRX
BQ340099
CE500599
AL120075
BF399610
CE336550
                                                                                                                                                                                                                                                            AY408064
CNS059UA
BI033106
CNS03ZII
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BI033106 MR4-NN020
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AK033805 Mus muscu
BU411177 603153320
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AL192822 Tetraodon
BQ340099 MR4-NN020
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AL120075 DKFZD761M
BF399610 UI-R-CA0-
CE336550 tigr-gss-
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45	44	43	42	41	40	39	38	37	36	3 5	34	33	32	<u>3</u> 1	30	29	28	27	26	25
262.6	264.8	279.2	283	294.8	298.2	304.8	308.6	310.6	315.4	327.8	348	352.2	353.6	357.4	370	371.4	377	378.4	399.8	403.6
12.4	12.5	13.2	13.3	13.9	14.1	14.4	14.5	14.6	14.9	15.5	16.4	16.6	16.7	16.9	17.4	17.5	17.8	17.8	18.8	19.0
477	374	814	595	435	352	796	594	576	477	471	647	956	600	723	715	753	679	698	463	636
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CO299664	AV604342	CF530818	CR540971	AI939560	CB780433	BU342672	BP209965	AZ449487	CR790592	AI369146	BB625540	CA477676	CR548281	CO393575	CB167795	CN220459	BB625814	BM947382	CD804043	CF897059
CO299664 E	AV604342 I	CF530818 L	CR540971 I	AI939560 c	CB780433 F	BU342672 6	BP209965 E	AZ449487 J	CR790592 I	AI369146 c	BB625540 E	CA477676 P	CR548281 I	CO393575 F	CB167795 F	CN220459 F	BB625814 E	BM947382 U	CD804043 U	CF897059 A
EK176303.	AV604342	UI-M-GH0-	DKFZp459A	qy74f11.x	AMGNNUC:S	603519328	BP209965	1M0247E16	DKFZp459M	qy74f11.x	BB625540	AGENCOURT	DKFZp459P	AGENCOURT	FBB603000	RJA066A09	BB625814	UI-M-EGOP	UI-M-GVO-	A0219E07-

## ALIGNMENTS

RESULT 1

Qy	Query Best I Match	ORIGIN	gene		801	FEATURES	COMMENT	TITLE				AUTHORS		DURNAL	TITLE			AUTHORS	· REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	· Artibau
73 ATGGCGGCCGGAGTTGCGGCCTGGCCTGTTTTGCCCCGGGCTGCGGCCATCGGGTGGATG 132	Query Match 86.7%; Score 1839.2; DB 9; Length 1911; Best Local Similarity 97.0%; Pred. No. 0; Matches 1908; Conservative 0; Mismatches 3; Indels 57; Gaps 1;	/locus_tag="HCM6847"		/organism="Homo sapiens"	source 11911		These sequences were made by sequencing genomic exons and ordering them based on alignment.	Direct Submission VI. Submitted (16-NOV-2003) Celera Genomics. 45 West Gude Drive,	Adams, M.D. and Cargill, M.	Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,	Todd.M.A. Tanenbaum.D.M. Civello.D.R. Lu.F.		٠ ا د	_	Inferring nonneutral evolution from human-chimp-mouse orthologous	Adams, M.D. and Cargill, M.	Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,			Bukaryota; metazoa; chordata; crahrata; vertebrata; butereostomi; Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.			GSS.			genomic survey sequence.	Homo sapiens KCND3 gene, VIRTUAL TRANSCRIPT		

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973 TCCCGCCACTCCCAGGGCCTGCGGATCCTGGGCTACACACTGAAGAGCTGTGCCTCCGAA 1032	13   ATCATCGACGTGGTGGCCATCATGCCCTACTACATCGGTCTGGTCATGACCAACAACGAG 91	33 CGCTACTCGGTGGCCTTCTTCTGCCTGGACACGGCGTGCGT	613 CTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTCGGTCATCACCAAC 672	493 AGGGAGAACGCCGAGCGGCTCATGGACGACAACGACTCGGAGAACAACCAGGAGTCCATG 552	373 GGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGAGGAGGAGGAGCTGGCCTTC 432	253 TACCCGGACACCCTGCTGGGCAGCACGAGAAGGAGTTCTTCTACAACGAGGACACCAAG 312		:CGGAGTTGCGGCCTGGCTGCCTTTTGCCCGGGCTGCGGCCATCGGGT :CAACTGCCCCATGCCCCTGGCCCCGGCCGACAAGAACAAGCGGCAGGA
AY419308 LOCUS DEFINITION Pan troglodytes KCND3 gene, VIRTUAL TRANSCRIPT, partial sequence,  ACCESSION VERSION KEYWORDS SOURCE ORGANISM Pan troglodytes (chimpanzee) ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  REFERENCE 1 (bases 1 to 1911) AUTHORS Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,	QY 1933 CCAGCGCTAACCCCCAGAGGGGAAAGTCGGCCACCCCCTGCCAGGCCCAGGCCCAACACG 1992	Qy 1813 AGTGAGCAGCCCTCCCCTCACAACCAGTCGCTCCAGCCTTAATTTGAAAGCAGACGACGGA 1872	OY 1693 GGCCTCACTACCACCTGCTCCGTCGTAGTANGANGACCACACCTGCCCAATTCT 1/52	y 15/3 CGARCCICCACCAICANGAACCA CACAGITIA I GAIGAGCAGAIGII I MAGCAGAICIGC I LAGGACAGAIGII I MAGCAGAIGII I MAGCAGAIGII I MAGCAGAIGII I MAGCAGAIGII I MAGCAGAIGII I MAGCAGAIGII MAGCAGAIGAICAGAIGAIGII MAGCAGAIGII MAGCAGAIGAIGII MAGCAGAIGII	y 1453 GAAGAGACACATGGGCAAGACCACCTCATCAGAGAGCCAGCATCATCAGCAGAGCCAGCATGATCACCTGCTG b 1381 GAAGAGGAGCACATGGGGCAAGACCACCTCATCGAGAGCCAGCATCATCACCTGCTG b 1381 GAAGAGGAGCACATGGGGCAAGACCACCTCATCGAGAGCCAGCATCATCACCTGCTG  y 1513 CACTGCCTGGAAAAAACCACTGGGTTGTCCTATCTTGTGGATGATCCCCTGTTATCTGTA b 1441 CACTGCCTGGAAAAAACCACT	b 1261 GCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAACAGGCAGTTCGAATGCA  y 1393 TACCTGCACAGCAAGCGCAACGGGCTCCTCAACGAGGCGCTTGAACGGGCACCCCA	Db 1141 AAGATCTTCGGCTCCATCTGCCAGGTGAGTGGCGTCCATTGCCAGTCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTTAAACGCAGG 1332  Qy 1273 GTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAGAGCTGATAAACGCAGG 1332  Db 1201 GTGATTGTTTCCAACTTTAGCCGGGATCTACCACCAGAATCAGAGAGCTGATAAACGCAGG 1260  Qy 1333 GCACAAAAGAAAGGACCCGCCTTGCCAGGATCCGTGTGGCCAAAAACAGGCAGTTCGAATGCA 1392	у 1213

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553 CCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGGCCTTCGAGAACCCCCACACCAGCACG 612	361 TACGGCATCCTCCCGGAGATCATCGGGGACTACGACGAGGAGTACAAGGACCGCAAG 420 361 TACGGCAATCCTCCCCGAGATCATCGGGGACTACGACGAGGAGTACAAGGACCGCAAG 420 493 AGGGAGAACGCCGAGCGGCTCATGGACGACGACGACTCGGAGAACCAACC	41 GAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTTCTACCGCACG 30 73 GGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGACGACGAGCTGGCCTTC 43	253 TACCCGGACACCCTGCTGGGCAGCACGGAGAAGGAGTTCTTCTTCAACGAGGACACCAAG 312	3 CTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACCACGCTGGAGCGC 25 	133 CCGGTGGCCAACTGCCCCATGCCCCTGGCCCCGGCCGACAAGAACAAGCGGCAGGATGAG 192 61 CCGGTGGCCAACTGCCCCATGCCCCTGGCCCCGGCCGACAAGAACAAGCGGCAGGATGAG 120	3 ATGGCGGCCGGAGTTGCGGCCTGGCTTTTGCCCCGGGCTGCGCCATCGGGTGGATG 13	tch 83.0%; Score 1761.4; DB 9; Length 1911; al Similarity 93.1%; Pred. No. 0; 1832; Conservative 0; Mismatches 79; Indels 57; Gaps 1;	<1 >1911 /gene="KCND3" /locus_tag="HCM6847"	e 1. 1911 /organism="Pan troglodytes" /mol_type="genomic DNA" /dh xref="taxon:9598"	Rockville, MD 20850, USA These sequences were made by sequencing genomic exons and ordering them based on alignment.  Location/Onalifiers	Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  E Direct Submission  NAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,	14671302  (bases 1 to 1911)  Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  Clark,A.G., Tanenbaum,D.M., Civello,D.R., Li,F., Murchy,R.,	Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios Science 302 (5652), 1960-1963 (2003)
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1504 ATGGAGAGTTCAATGCAGAACTACCCATCCACAAGAAGTCCCTCACTGCCGAGCCCCCA 1563 1504 ATGGAGAGTTCAATGCCAGAACTACCCATCCACAAGAAGTCCCTCACTGCCCAGCCCCCCCC	441 CACTGCCTGGAAAAAACCACT 146  573 CGAACCTCCACCATCAAGAACCACGAGTTTATTGATGAGCAGATGTTTGAGCAGAACTGC 163	453 GAAGAGGAGCACATGGGCAAGACCACCTCACTCATCGAGAGCCAGCATCATCACCTGCTG 15	261 GCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAACAGGCAGTTCGAATGCA 132 261 TACCTGCACAGCAACGCGAACGGGCTCCTCAACGAGCGCTGGAGCTGACGGGCACCCCA 145	TGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAGAGCTGATAAACGCA 	3 AAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCATTGCCCTGCCAGT	153 ACCATTGTCACCATGACCACACTGGGATACGGAGACATGGTGCCTAAGACGATTGCAGGG 121 	1093 TATIGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCCTGCCTCGTTTTTGGTAC 1152	1033 CTGGGCTTTCTCTCTCTCCCCCACCATGGCCATCATCATCTTTGCCACTGTGATGTTT 1092	973 TCCCGCCACTCCCAGGGCCTGCGGATCCTGGGCTACACACTGAAGAGCTGTGCCTCCGAA 1032	913 GACGTGTCCGGCGCTTCGTCACGCTCCCGGGTCTTCCACGATCTTCAAGTTT 972	53 ATCATCGACGTGGTGGCCATCATGCCCTACTACATCGGTCTGGTCATGACCAACAACGAG 9	793 TACCTCCTGCGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCATCCGCAGCGTCATGAGC 852	733 CGCTACTCGGTGGCCTTCTTCTGCCTGGACACGGCGTGCGT

Query Matches  Qy  Db  Qy  Db	COMMENT FEATURES SOURCE Gene ORIGIN	TITLE JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL	RESULT 3 AY419309 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	B & B & B & B &
Watch Local Similarity 88.6%; Pred. No. 0; Local Similarity 88.6%; Pred. No. 0;  nes 1744; Conservative 0; Mismatches 167; Indels 57; Gaps 1;  73 ATGGCGGCCGGAGTTGCGGCCTGGCTGCTTTTGCCCGGGCTGCGCCATCGGGTGGATG 132	Rockville, MD 20850, USA These sequences were made by sequencing them based on alignment. Location/Qualifiers 11911 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" <1>1911 /gene="KCND3" /locus_tag="HCM6847"	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  Inferring nonneutral evolution from human-chimp-mouse orthogene trios Science 302 (5652), 1960-1963 (2003)  14671302  2 (bases 1 to 1911)  Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission  Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive	AY419309  AY419309  Mus musculus KCND3 gene, VIRTUAL TRANSCRIPT, part genomic survey sequence.  AY419309  AY419309.1 GI:39775266  GSS.  Mus musculus (house mouse)  Mus musculus  Eukaryota; Metazoa; Chordata; Craniata; Vertebrat Mammalia; Eutheria; Rodentia; Sciurognathi; Muric 1 (bases 1 to 1911)  Clark & G. Glanowski S. Nielson B. Thomas B.	1813 AGTGAGCAGCCCTCCCTCACAACCAGTCGCTCCAGCCTTAATTTGAAAGCAGACGACGGA 1872
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1093 TATGCCGAGAAGGGTCCTCGGCCAGCAAGTTCACAAGCATCCCTGCCTCTCTTTGGTAC 1152	13 GACGTGTCCGGCGCCTTCGTCACGCTCCCGGTCTTCCGCGTCTTCAGGATCTTCAAGTTT 972	ol diddiddadacddidcichiccididcicdidcichiddadadadadadadadadadadadadadadadadadad	493 AGGGAGAACGCCGAGCGGCTCATGGACGACGACTCGGAGAACAACCAGGAGTCCATG 552	TACCCGGACACCCTGCTGGGCAGCACGGAGAAGGAGTTCTTCTAACGAGGACACCAAG 312

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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AK033962
3730 bp mRNA linear HTC 03-APR-200. Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330129C02 product:potassium voltage-gated channel, Shal-related family, member 3, full insert sequence.
                                                                                                                                                                                         Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999)
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-JUL-2001) Yoshihide RIKEN (16-JUL-2001) Yoshihide Exploration Research Group, RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Exploration Laboratory in Riken to the following Sciences Center and Genome Laboratory in Riken to the following Sciences Center and Genome Laboratory in Riken to the following Sciences Center and Genome Science Laboratory in Riken to the following Sciences Center and Genome Science Laboratory in Riken to the following Sciences Center and Genome Science Laboratory in Riken to the following Sciences Center and Genome Science Laboratory in Riken to the following Sciences Center and Genome Science Laboratory in Riken to the following Sciences Center and Genome Science Laboratory in Riken to the following Sciences Center and Genome Science Laboratory in Riken to the following Sciences Center and Genome Science Laboratory in Riken to the following Sciences Center and Genome Science Laboratory in Riken to the following Sciences Center and Genome Sciences Center and Genome Sciences Center and Genome Sciences Center and Genome Science Laboratory in Riken to the following Sciences Center and Genome Sciences Center and Genome Sciences Center and Genome Sciences Center and Genome Center and Genome Sciences Center and Genome Sciences Center and Genome Center and Geno
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Please visit ....
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Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
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putative"
                                                                                                                                                                                                                                          /mol_type="mRNA"
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AK032268.1 GI:26328092
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Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordat
Mammalia; Eutheria; Rodenti
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 Carninci,
Itoh, M.,
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                                                                                                                                                                                                                                                                  AK032268 2997 bp mRNA linear HTC 03-APR-2004 Mus musculus adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430513P12 product:potassium channel Kv4.2 mRNA, full insert sequence.
                                                                                  Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Xira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                      prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
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                                                                                                                                                                                                                                                                The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Functional annotation of a full-length mouse cDNA collection sature 409, 685-690 (2001)
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                                          /dev_stage="adult"
982._.2874
                                                                                                                               /db_xref="FANTOM_DB:6430513P12"
/db_xref="taxon:10090"
/clone="6430513P12"
/note="unnamed protein product; potassium channel Kv4.2 nRNA (GB|AF107780, evidence: BLASTN, 100%, match=1893)
                                                                      tissue_type="olfactory brain"/clone_lib="RIKEN_full-length enriched mouse cDNA library"
                                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6J"
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ry Match 43.4%; Score 920.2; DB 3; Length 2997; t Local Similarity 70.0%; Pred. No. 8.2e-205; ches 1344; Conservative 0; Mismatches 508; Indels 69; Gaps 5;
53 GCCCAAGAGCTGGAGTCACCATGGCGGCCGGAGTTGCGGCCTGGCTGCCTTTTTGCCCGGG 112
113 CTGCGGCCATCGGGTGGATGCCGGTGGCCAACTGCCCCATGCCCCTGGCCCCGGCCGACA 172
173 AGAACAAGCGGCAGGATGAGCTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGA 229
230 CCTGGAGGACCACGCTGGAGCGCTACCCCGGACACCCTGCTGGGCAGCACGGAGAAGGAGT 289
290 TCTTCTTCAACGAGGACACCAAGGAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCT 349
350 GCGTGCTCAACTTCTACCGCACGGGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTG 409 
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470 ACGAGGAGTACAAGGACCGCAAGAGGGAGAACGCCGAGCGGCTCATGGACGACAACGACT 529
530 CGGAGAACCAGGAGTCCATGCCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGG 586
587 CCTTCGAGAACCCCCACACCAGCACGCTGGCCCTGGTCTTCTACTACGTGACTGGCTTCT 646
647 TCATCGCTGTCTCGGTCATCACCAACGTGGTGGAGACGGTGCCGTGCGGCACGGTCCCGG 706
707 GCAGCAAGGAGCTGCCGTGCGGGGAGCGCTACTCGGTGGCCTTCTTCTGCCTGGACA 763
764 CEGEGTGCGTCATGATCTTCACCGTGGAGTACCTCCTGCGGGCTCTTCGCGGCTCCCAGCC 823

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AY406812
AY406812.1 GI:39762783
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(bases 1 to 1893)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (16-NOV-2003) Celera Genomics,
Rockville, MD 20850, USA
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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Science 302 (5652), 1960-1963
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Location/Qualifiers
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                      genomic survey sequence.

N AY406814

AY406814.1 GI:39762785

GSS.

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 1893)

E 1 (bases 1 to 1893)

E Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
                                                              Submitted (16-NOV-2003) Celera Genomi Rockville, MD 20850, USA
This sequence was made by sequencing them based on alignment.
Location/Qualifiers
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Science 302 (5652), 1960-1963
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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QY 904 AACAACGAGGACGTGTCCGGGCGCCTTCGTCACGCTCTCCGGGTCTTCAGGATC 963	Qy 784 ACCGTGGAGTACCTCCTGCGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCATCCGCAGC 843	Qy 667 ACCAACGTGGTGGAGACGGTGCCGTGCGGCACGGTCCCGGGCAGCAAGGAGCTGCCG 723	Qy  548 -CCATGCCCTCGCTCAGCTTCCGCCAGACCATGTGCGGGCCTTCGAGAACCCCCACACC 606	Qy 430 TTCTACGGCATCCTCCCGGAGATCATCGGGGACTGCTACGAGGAGTACAAGGACCGC 489	Qy  310 AAGGAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTTCTACCGC 369	Qy 190 GAGCTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACCACGCTGGAG 249	Similarity 67.1%; Pred. No. 1.4e-197; 6; Conservative 0; Mismatches 556; Indels 6 Argacagacagarracagacargacargacaracagacaga	gene <1>1893 /gene="KCND2" /locus_tag="HCM2682" uery Match 41.9%; Score 889.2; DB 9
RESULT 8 AY408063 AY408063 LOCUS AY408063 DEFINITION Homo sapiens KCND1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. ACCESSION AY408063 VERSION AY408063.1 GI:39764034 KEYWORDS GSS.		1744   CCCARTCTAACCTGCCAGCTACTCGCCTGCGCAGCAGCAGCAGCTCAGCAGCAGCAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1501 GAAAGCTGCATGGAAGTTGCCACCGTCAATCGCCATCAAGTCACAGTCCCTCTCTCC 156  1501 GAAAGCTGCATGGAAGTTGCCACCGTCAATCGCCCATCAAGTCACAGTCCCTCTCTCC 156  1684 AGCCACCCAGGCCTCACTACCACCTGCTGCTCCCGTAGTAAGAAGACCACACACA	1381 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN		Qy 1264 CCAGTCCTGTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGACAGA	1021 ĠTTATĠTTCTACĠCAĠĀĠĀĠĠĠĊŦĊŢŦĊAĠCĀĀĠĊĀĠĊĀĠĊĀŦĊĊĊĠĠĊAĠĊC 10 1144 TTTTGGTACACCATGTCACCATGACCACACTGGGATACGGAGACATGGTGCCTAAGACG 12	024 GCCTCCGAACTGGGCTTTCTCTCTCTCTCCCTCACCATGGCCATCATCATCTTTTGCCACT 10 

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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Submitted (16-NOV-2003) Celera
Rockville, MD 20850, USA
This sequence was made by seque
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Science 302 (5652), 1960-1963
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1 (bases 1 to 1944)

Todark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
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                                   CCCTCGCT-----CAGCTTCCGCCAGACCATGTGGCGGGCCTTCGAGAACCCCCCAC
                                                                                                                                        TACGGCCTGGTTCCCGAGCTAGTCGGTGACTGCTTGCAGAGAGTATCGGGACCGAAAG
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                   GCCCTGCCAGCAGGCAGCTCCCTGCGGCAGCGGCTCTGGCGGGCCTTCGAGAATCCACAC
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/locus_tag="HCM3099"
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Pred. No. 6.3e-176;
0; Mismatches 375; Indels
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Mus musculus KCND1 gene, v
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                                                               1956 bp
, VIRTUAL
                                                            DNA linear GSS 15-DEC-2003 TRANSCRIPT, partial sequence,
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960 1017 957

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840 897 780 837 720

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1200 1257 1140

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JOURNAL
PUBMED
REFERENCE
AUTHORS
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Best Local Similarity
Matches 1059; Conserv
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 1956)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 1956)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-NOV-2003) Celera Genomi
Rockville, MD 20850, USA
This sequence was made by sequencing
them based on alignment.
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Science 302 (5652), 1960-1963 (2003)
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                                                                                        AAGGAAAACGCAGAGCGCCTGGCAGAAGATGAGGAGGCTGAGCCAGGCCGGGGAAGGTCCA
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/locus_tag="HCM3099"
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71.8%;
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Pred. No. 3.4e-167;
0; Mismatches 392;
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                                                                   AY406813 1893 bp DNA linear GSS 15-DEC-2003 Pan troglodytes KCND2 gene, VIRTUAL TRANSCRIPT, partial sequence,
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1501 GAAAGCTGCATGGAAGTTGCAACTGTTAATCGTCCTTCAAGTCACAGTCNNNCACTGTCT 1560 1684 AGCCACCCAGGCCTCACTACCACCTGCTGCTCCCGTCGTAGTAAGAAGACCACACACCTG 1743	1624 CAGAACTGCATGGAGAGTTCAATGCAGAACTACCACAAGAACTACGAGAACAAGTCCTTCGACAAGTCCCTCACTGTCC 1683	TTATCTGTACGAACCTCCACCATCAAGAACCACGAGTTTATTGATGAGGAGATGTTTGAG 1	NININININININININININININININININININI	1372CAGNNNNNN 1380 1504 CACCTGCTGCACTGCCTGGAAAAAACCACTGGGTTGTCCTATCTTGTGGATGATCCCCTG 1563	GGCACCCCAGAAGAGGAGCACATGGGCAAGACCACCTCACTCA		1261 AMACGAMGGGCACAAAAAGAAAGCTAGACTGGCCAGGATCCGGGCAGCCAAAAGCGGAAGC 1320 1384 TCGAATGCATACCTGCACAGCAAGCGCAACGGCCAACGAGGCGCTGGAGCTGACG 1443	AAACGCAGGCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAACAGGCAGT	1264 CCAGTCCCTGTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAGGAGCTGAT 1323	ATAGCAGGGAAGATTTTTGGTTCTATCTGTTCACTGAGTGGGGTCTTGGTCATTGCTCTA	1204 ATTGCAGGGAAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCATTGCCCTG 1263	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	TTTTGGTACACCATTGTCACCATGACCACACTGGGATACGGAGACATGGTGCCTAAGACG	NANNANANANANANANANANANANANANANANANANAN		1024 GCCTCGAACTGGGCTTTCTTCTCTTCTCCCTCACCATGGCCATCATCATCTTTGCCACT 1083	TTTAAGTTTTCCCGCCACTCTCAAGGCCTGCGCATCCTGGGGGTACACACTGAAGAGTTGT	964 TTCAAGTTTTCCCGCCACTCCCAGGGCCTGCGGATCCTGGGCTACACACTGAAGAGCTGT 102:	GACAATGAGGACGTCAGCGGAGCCTTTGTCACACTCCGAGTCTTCCGGGTCTTCAGGATC	AACAACGAGGACGTGTCCGGCGCCTTCGTCACGCTCCGGGGTCTTCCGCGTCTTCAGGATC	844 GICATGAGCATCATCGACGTGGTGGCCATCATGCCTACATCGGTCTGGTCATGACC 903	721 ACAGTTGAGTATTTGCTTCGCCTGGCTGCAGCGCCTAGTCGTTACCGTTTTGTGCGTAGT 780	784 ACCGTGGAGTACCTCCTGCGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCATCCGCAGC 843	661 NGTGGAGAGCGGTATGCTGTGGCNNNNTTCTGCTTGGACACGGCCTGCGTCATGATCTTC 720	724 TGCGGGGAGCGCTACTCGGTGGCCTTCTTCTGCCTGGACACGGGCGTGCGT	601 NININININININININININININININININININI	664 ÁTCACCAACGTGGTGGAGACGGTGCCGTGCGGCACGGTCCCGGGCAGCAAGGAGCTGCCG 723	541 NININININININININININININININININININI

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	133 CCGGTGGCCAACTGCCCCATGCCCCTGGCCCGGCCGAAGAACAAGCGAGGAGAGAGA	ATGGCNNCAGGCCTGGCNNNGTGGCTGCCTTTTGCCCCGGGCAGCAGCAGTGGGCTGCCTG	13	Match 30.5%; Score 647.8; DB 9; Length 1939; ocal Similarity 58.6%; Pred. No. 6.5e-141; s 864; Conservative 0; Mismatches 587; Indels 24; Gaps 2;		/Yerre="NcMD1" /locus_tag="HCM3099"	<1 >1939	/organizes= / the story con / toge see see see see see see see see see s	Ф	based on alignment.	Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ord		Perriera, S., Wang, G., Zheng, X.H., White, T Adams, M.D. and Cargill, M.	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariw Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B	14671302 2 (bases 1 to 1939)	gene trios Science 302 (5652), 1960-1963 (2003)	D. and Cargill, M. g nonneutral evolution from human-chim	D.R., Lu,F., M hite,T.J., Sni	., Thomas, P	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pan.	Pan troglodytes (CHIMPANIZEE)	V† (	AY408064 AY408064.1 GI:39764035	genomic survey sequence.	AY408064 1939 bp DNA linear GSS		1801 CCAACACCTCCAGTAACCACACAGAAGGAGACGATAGGCCA 1842	1924 CCCACTCCCCAGCGCTAACCCCCAGAGGGGGGAAAGTCGGCCA 1965		1864 GACGACGGACTGAGACCAAACTGCAAAACATCCCCAGATCACCACAGCCATCATCAGCATC 1923	1804 ATCCAGGCAGTGAGCAGCCCTCCCCTCACAACCAGTCGCTCCAGCCTTAATTTGAAAGCA 1863	621 CCAAATGCCAATGTATCAGGAAGCCATCAAGGTAGTATACAAGAACTCAGCACGATTCAG 168	1744 CCCAATTCTAACCTGCCAGCTACTCGCCTGCGCAGCATGCAAGAGCTCAGCACGATCCAC 1803	
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This sequence is a single read and was generated as part of a lar scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Characterization and repeat analysis of the compact genome of treshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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nigroviridis genome survey sequence T3 end of clone
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                                                                             organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
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Pred. No. 2.7e-124;
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BI033106 567 bp mRNA linear MR4-NN0205-310101-201-e10 NN0205 Homo sapiens cDNA,

EST 14-JUN-2001

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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-NN0205-
310101-201-e10&t3=2001-01-31&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: nervous normal; Vector: puc18; Site 1: Smal; Site 2: Smal; A mini-Tibrary was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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v_stage="Adult"
one_lib="NN0205"
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Pred. No. 1.1e-118;
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Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Meopterygii; Teleostei; Euteleostei; Neoteleostei;
Actinopterygii; Neopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                              This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                         /organism="Tetraodon ni
/mol_type="genomic DNA"
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Direct Submission

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                             LL Nature 420, 563-573 (2002)

B 6 (bases 1 to 3302)

B Adachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nashi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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CTTTCTTCTCTCTCCCTCACCATGGCCATCATCATCTTTGCCACTGTGATGTTTTATGC
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ADKRRAQOKVRLARIRLAKSGTTNAFLQYKQNGGLBGSGGGGMLCVRSRSAFEQOH
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Search completed: April 5, 2005, 18:33:20 Job time : 6237.08 secs Ś 밁 ঠ В ঠ 밁 δ 밁 δ 밁 Ś 밁 ঠ 밁 S 밁

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47.9 47.8 47.7	48.5 48.5 48.4	51.2 50.8 50.0 49.9 49.7 48.7	.7	80.3 79:6 77.4 77.3 76.4 75.7
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## ALIGNMENTS

RESULT 1 AN371147 LOCUS LOCUS AR371147 LOCUS DEFINITION Sequence 3 from patent US 6385477. ACCESSION AR371347.1 GI:34608279 KEYWORDS SOURCE ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 2064) LOCATION Unclassified. REFERENCE 1 (bases 1 to 2064) REFERENCE 1 (bases 1 to						•	
AR371347  Sequence 3 from patent US 6395477.  AR371347.  AR371347.1 GI:34608279  Unknown. Unclassified. 1 (bases 1 to 2064) 1 (cockett,M.I., Dilks,D.W., Ling,HP.C. and Sokol.P.T. Human potassium channel polynucleotide and polypeptides thereof Patent: US 6395477-A 3 28-MAY-2002; Location/Qualifiers 1 . 2064  (organism="unknown" /mol_type="genomic DNA"  tch tch tal similarity 100.0%; Score 2064; DB 6; Length 2064; al Similarity 100.0%; Pred. No. 5.5e-308; 2064; Conservative 0; Mismatches 0; Indels 0; 1 GATTTGCTGAACTAACTCCAAGCTGGTGTGCCTAGCGTCCGGCGGGTGCCGGC [				Db Qq	Qy .		RESULT 1 AR371347 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES sourC
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Cockett, M.I., Dilks, D.W., Ling, H.-P.C.
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Cloning and expression of the human kv4.3 potassium channel
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Gene structures and expression profiles of three human KCND potassium channels mediating A-type currents I(TO) and I(SA)
Genomics 64 (2), 144-154 (2000)
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Homo sapiens Shal-related potassium
long splice variant, complete cds.
AF120491
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Zhu,X.R., Waldschuetz,R., Isbrandt,D., Sauter,K. and Direct Submission
Submitted (15-JAN-1999) ZMNH, Institut fuer Neurale
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 CAGGAGTCCATGCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGGCCTTCGAGAACCCC
                                                              AAGGACCGCAAGAGGGAGAACGCCGAGCGGCTCATGGACGACAACGACTCGGAGAAACAAC
                                                                                                                                                 GAGCTGGCCTTCTACGGCATCCTCCCGGAGATCATCGGGGACTGCTGCTACGAGGAGTAC
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PSLSFRQTWWRAFENPHTSTLALVFYYVTGFFIAVSVITNVVETVPCGTVPGSKELPC
GERYSVAFFCLDTACVMIFTGEYLLRLFAAPSRYRFIRSVMSIIDVVAINFYIGLVM
TNNEDVSGAFVTLRVFRVFRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIII
FATVMFYAEKGSSASKFTSIPASFWYTIVTMTTLGYGDWLKTIAGKIFGSICSLSGV
LVIALPVPVIVSNFSRIYHQNQRADKRRAQKXARLARIRVAKTGSSNAYLHSKRNGLL
NEALELTGTPEEEHWGKTTSLIESQHHHLLHCLEKTTGLSYLVDDPLLSVRTSTIKNH
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LRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDGLRPNCKTSQITTAIISIPTPPALT
PEGESRPPPASPGPNTNIPSITSNVVKVSVL"
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Homo sapiens Kv.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1911)
Kong, W. and Tomaselli, G.F.
Direct Submission
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AF048712.1
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Oy 913 GAC     Db 841 GAC	Qy     793 TACCTV       Db     721 TACCTV       QY     853 ATCATV       Db     781 ATCATV	Oy 733 CGC	Qy 673 GTGG      Db 601 GTGG	Qy 613 CTGGC	Oy 553 CCCTO	Qy 493 AGG     Db 421 AGG	Qy 433 TAC	Qy 373 GGG 	Qy 313 GAG     Db 241 GAG	Qy 253 TAC      Db 181 TAC	Qy 193 CTG          Db 121 CTG	Qy 133 CCG 	Qy 73 ATGG	Query Match Best Local Simi Matches 1908;	ORIGIN	
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TTCAGGATCTTCAAGTTT 9	ATCCGCAGCGTCATGAGC 8	ATGATCI	reccerecee	GTCTCGGTCATCACCAAC 6	AACCCCCACACCAGCACG 6	AACAACCÄGGAGTCCATG 5	AGTACAAGGACCGCAAG 	ACGACGAGCTGGCCTTC	FIGCTCAACITCTACCGCACG	GTTCTTCAACGAGGACACCAAG :	CCTGGAGGACCACGCTGGAGCGC 2	CGACAAGAACAAGCGGCAGGATGAG : 	CGGCCATCGGGTGGATG	Length 1911; Indels 0; Gaps	PATRLRSMQELST HIQGS PALTPEGESRPPPASPGPN	TNNEDVSGAFVTLRVFRVFRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIII FATVMFYAEKGSSASKFTSIPASFWYTIVTMTTLGYGDMVLKTIAGKIFGSICSLSGV LVIALPVPVIVSNFSRIYHQNQRADKRRAQKKARLARIRVAKTGSSNAYLHSKRNGLL NEALELTGTPEEEHMGKTTSLIESOHHHLLHCLEKTTNHEFIDEOMFEONCMESSSMON
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PAT 21-JAN-200	  GCCCCAAC 1983	AGCATCCCCACT 1            AGCATCCCCACT 1	AAAGCAGACGAC 1            AAAGCAGACGAC 1	ATCCACATCCAG 1						AGTTCGAATGCA 1	AACGCAGG	CAGTCCCT	TTGCAGGG	TCGTTTTGGTAC 1	ACTGTGATGTTT 1	TGTGCCTCCGAA           TGTGCCTCCGAA

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793 TACCTCCTGCGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCATCCGCAGCGTCATGAGC 852	601 GIGGIGGAGACGGIGCGGIGCGGGACGGICCCGGGCAGGAAGGA	613 CTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTCGGTCATCACCAAC 672	53 CCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGGCCTTCGAGAACCCCCACACCAGCACG 6	93 AGGGAGAACGCCGAGCGGCTCATGGACGACAACGACTCGGAGAACAACCAGGAGTCCATG 55 	433 TACGGCATCCTCCCGGAGATCATCGGGGGACTGCTGCTACGAGGAGTACAAGGACCGCAAG 492	373 GGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGACGAGCTGGCCTTC 432	13 GAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTTCTACCGCACG 3	TACCCGGACACCCTGCTGGGCAGCACGGAGAAGGAGTTCTTCTTCAACGAGGACACCAAG 31 	193 CTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACCACGCTGGAGCGC 252	133 CCGGTGGCCAACTGCCCCATGCCCCTGGCCCCGGCCGACAAGAACAAGCGGCAGGATGAG 192	73 ATGGCGGCCGGAGTTGCGGCCTGGCTGCCTTTTGCCCGGGCTGCGGCCATCGGGTGGATG 132	atch 92.3%; Score 1905; DB 6; Length 2104; cal Similarity 99.2%; Pred. No. 1.6e-283; 1914; Conservative 0; Mismatches 15; Indels 0; Gaps 0;	/organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644"	2	unidentified unclassified.  1 (bases 1 to 2104) Bril,A.M. and Calmels,T.P.	A85164 A85164.1 GI:6733867 unidentified
. ט	S B 8	א מ מ	S B 8	dg Qy	g	g S	D Qy	Db Qy	유 상	dg Qy	dg VQ	gg Qy	Qy db	d d	В б	B <i>Q</i>
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26 A B A	Qy Db	D Qy	D Qy	Qy Db	Qy Db	D Q	Qy Db	B &	Query Best I Matche		TITLE JOURNAL	ORGANISM REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE	RESULT 7 AR204884 LOCUS DEFINITI	ďa	S B S
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Db Db	Q B Q	B 8	Qy da	D Qy	D Q	Db	da Vo	g gy	D QY	Db Qy	D Qy	Qγ	ОУ	Qy. Db	рь	Qy Db
	73 TGCATGGAGAGTTCAATGCAGAACTACCCATCCACAAGAAGTCCCTCACTGTCCAGCCAC 16	.513 CACTGCCTGGAAAAAACCACTAACCACGAGTTTATTGATGATGAGGAGATGTTTGAGCAGAAC 1	453 GAAGAGGAGCACATGGGCAAGACCACCTCACTCATCGAGAGCCAGCATCATCATCACCTGCTG 15	393 TACCTGCACAGCAAGCGCAACGGGCTCCTCAACGAGGCGCTGGAGCTGACGGGCACCCCA 14	333 GCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAACAGGCAGTTCGAATGCA 13	273 GTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAGAGCTGATAAACGCAGG 13	213 AAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCATTGCCCTGCCAGTCCCT 12	3 ACCATTGTCACCATGACCACACTGGGATACGGAGACATGGTGCCTAAGACGATTGCAGGG 1	93 TATGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCCTGCCTCGTTTTGGTAC 11	033 CTGGGCTTTCTTCTCTCTCCCTCACCATGGCCATCATCATCTTTGCCACTGTGATGTTT 10 	973 TCCCGCCACTCCCAGGGCCTGCGGATCCTGGGCTACACACTGAAGAGCTGTGCCTCCGAA 103 	913 GACGIGICCGGCGCCTTCGTCACGCTCCGGGICTTCCGCGTCTTCAGGATCTTCAAGTTT 972	853 ATCATCGACGTGGTGGCCATCATGCCCTACTACATCGGTCTGGTCATGACCAACAACGAG 912	.793 TACCTCCTGCGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCATCCGCAGCGTCATGAGC 852	733 CGCTACTCGGTGGCCTTCTTCTGCCTGGACACGGCGTGCGT	

Query Match	VE NV LLH YP NE	/mol/db//tis/tis/cod/pro//pro//pro//db///cod//pro//pro//pro//pro//pro//pro//pro//p	REFERENCE 2 (bases 1 AUTHORS Calmels, T.P TITLE Direct Subm JOURNAL Submitted ( Beecham, 4: FEATURES SOURCE 1.		AF205856 LOCUS LOCUS AF205856 LOCUS AF205856 DEFINITION COMMPLE Cds. ACCESSION AF205856 VERSION AF205856.1 G KEYWORDS SOURCE ORGANISM Homo sapiens	1861 1993 1921	Qy       1813 GGACTGAGA                          Db       1741 GGACTGAGA         Qy       1873 CCCCCAGCGG                         Db       1801 CCCCCAGCGG         Qy       1933 ACGAACATT
92.2%; Score 1903; DI	anslation="MAAGVAAWLPFARIGRRFQTWRTTLERYPDTLLGSTEKIGRRFQTWRTTLERYPDTLLGSTEKIGRRFQTWRTTLERYPDTLLGSTEKIGRRFQTWRTAFENPHTSTLALVFYYTAFFCLDTACVMIFTVEYLLRLIEDVSGAFVTLRVFRVFRIFKFSRHYTVMFYAEKGSSASKFTSIPASFWYTVMFYAEKGSSASKFTSIPASFWYTTALPVPVIVSNFSRIYHQNQRADKRILLELTGTPEEEHMGKTTSLIESQHHITRSPSLSSHPGLTTTCCSRRSKKTTSRSSLNLKADDGLRPNCKTSQITTYSRSSLNLKADDGLRPNCKTSQITTYSRSSLNLKADDGLRPNCKTSQITTYSNVVKVSAL"	/mol_type="mRNA" /db_xref="taxon:9606" /tissue_type="heart" 1. ,1911 1. ,1911 1. ,opin="transient outward/function="transient outward/functe="similar to cardiac ITV/codon_start=1 /product="potassium ionic chi/prodein_id="AAF70924.1" /protein_id="AAF70924.1" /db_xref="GI:6644150"	Calmels, T.P.G., Faivre, JF., Javre, J. Calmels, T.P.G., Faivre, JF., Javre, J. Direct Submission Submitted (17-NOV-1999) Cardiovascular Beecham, 4 Rue du Chesnay Beauregard, Location/Qualifiers 11911 e /organism="Homo sapiens"	Metazoa; Chordata; Craniata; Veriutheria; Primates; Catarrhini; H. ( to 1911) P.G., Faivre, JF., Javre, JL., ( nort Human Isoforms of the Kv4.3 ( Electrophysiology, Pharmacology )	1911 bp um ionic channe 49		CAAACTGCAAAACATCCCAGATCAC 
B 9; Length 1911;	/translation="MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKRQDELIVL NVSGRRFQTWRTTLERYPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGK LHYPRYECISAYDDELAFYGILPEIIGDCCYEEYKDRKRENAERLMDDNDSENNQESM PSLSFRQTMWRAFENPHTSTLALVFYYVTGFFIAVSVIITNVVETVPCGTVPGSKELPC GERYSVAFFCLDTACVMIFTVEYLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVM TNNEDVSGAFVTLRVFRVFRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIII FATVMFYAEKGSSASKFTSIPASFWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGV LVIALPVPVIVSNFSRIYHQNQRADKRRAQKKARLARIIVAKTGSSNAYLHSKRNGLL NEALELTGTPEEEHMGKTTSLIESQHHHLLHCLEKTTNHEFIDEQMFEQNCMESSMON YPSTRSPSLSSHPGLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPS LTTSRSSLNLKADDGLRPNCKTSQITTAIISIPTPPALTPEGESRPPPASPGPNTNIP SIASNVVKVSAL"	rd potassium channel" ITO1" channel Kv4.3 short isoform"	JL. and Bril,A. ar Pharmacology, SmithKline , Saint Gregoire 35760, Franc	tebrata; Euteleostomiominidae; Homo. Cheval,B., Rouanet,S. Channel: Cloning, and Phosphorylation	mRNA linear PRI 29-DEC-1 1 Kv4.3 short isoform mRNA,		
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Qy 1093 TA7	913 G 973 T 961 C-C T	661 CC 793 TZ 721 TZ 853 AJ 781 AJ	OY 541 CTGGG OY 673 GTGGG OY 671 GTGGG OY 733 CGCT1	493 AC 421 AC 42	241 GA 373 GG 301 GG 433 TA 433 TA 361 TA	21 CT	73 <i>I</i> 1 <i>I</i> 133 ( 61 ( 193 (
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ACCESSION
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KEYWORDS
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Homo sapiens voltage gavariant (Kv4.3) mRNA, AF187963
AF187963.1 GI:6007794
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2041)
Dilks,D., Ling,H.P., Cockett,M., Sokol,P. and Numann,R.
                                                                         Homo sapiens (human)
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Dilks,D.W., Ling,H.-P., Cockett,M., Sokol,P. and Numann,R.
Direct Submission
Submitted (17-SEP-1999) Neuroscience, Wyeth-Ayerst Research,
8000, Room 1119A, Princeton, NJ 08543-8000, USA
Location/Qualifiers
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/COGON STATE-1
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/protein id="AAF01044.1"
/db_xref="GI:6007795"
/translation="MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKRQDELIVL
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PSLSFRQTWWRAFENPHTSTLALVFYYVTGFFIAVSVITNVVETVPCGTVPGSKELPC
GERYSVAFFCLDTACVMIFTVEYLLRLFAAPSRYRFIRSVMSIIDVVALMFYYIGLVM
TNNEDVSGAFVTLRVFRVFRIFFSFRHSQGLRILGYTLKSCASELGFLLFSLTMAIII
FATVMFYAEKGSSASKFTSIPASFWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGV
LVIALPVPVIVSNFSGIYHQNQRADKRRAQKXARLARIRVAKTGSSNAYLHSKRNGLL
NGALELTGTPEEEHMGKTTSLIESQHHHLLHCLEKTTGLSYLVDDPLLSVRTSTIKNH
EFIDEQMFEQNCMESSMQNYPSQRSPSLSSHPGLTTTCCSRRSKKTTHLPNSNLPDTR
LRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDGLRPNCKTSQITTAIISIPTPPALT
PEGESRPPPASPGPNTNIPSIASNVVKVSVL"
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CATCACCTGCTGCACTGCCTGGAAAAAACCACTGGGTTGTCCTATCTTGTGGATGATCCC
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Bril,A.M. and Calmels,T.P.
KV POTASSIUM CHANNEL POLYPEPTIDES AND POLYNUCLEOTIDES
Patent: WO 9842833-A 5 01-OCT-1998;
BRIL ANTOINE MICHEL ALAIN (FR); CALMELS THIERRY PAUL (
Location/Qualifiers
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                                           CCGGTGGCCAACTGCCCCATGCCCCTGGCCCCGGCCGACAAGAACAAGCAGCGGCAGGATGAG
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Score 1897; DB 6; Pred. No. 2.7e-282;

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RS Bril, A.Michel. Alain., Calmels, T. Paul. Gerard.,

Faivre, J.-F. Simon. Pierre, Javre, J.-L. and Rouanet, S.

E Kv potassium channel polypeptides and polynucleotides

WAL Patent: US 6368823-A 5 09-APR-2002;

Location/Qualifiers

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DEFINITION Homo saptens Kv4.3 poctors mRNA, complete cds. ACCESSION AF048713 VERSION AF048713.1 GI:2935435	1033 CTGGGCTTTCTCTCTCTCCCTCACCATGGCCATCATCATCTTTGCCACTGTGATGTTT 1092	음 성
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1861 ACGAACATTC	853 ATCATCGACGTGGTGGCCATCATGCCCTACTACATCGGTCTGGTCATGACCAACAACGAG 912	유 성
1801	793 TACCTCCTGCGGCTCCTTCGCGGCTCCCAGCCGCTACCGCTTCATCCGCAGCGTCATGAGC 852	음 성
1813	733 CGCTACTCGGTGGCCTTCTTCTGCCTGGACACGGCGTGCGT	음 성
1681	673 GTGGTGGAGACGGTGCCGTGCGGCACGGTCCCCGGCCAGCAAGGAGCTGCCGTGCGGGGAG 732	유
1621	613 CTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTCGGTCATCACCAAC 672	음 성
1561	553 CCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGGCCTTCGAGAACCCCCACACCAGCACG 612	음 성
1501 1	493 AGGGAGAACGCCGAGCGGCTCATGGACGACAACGACTCGGAGAACAACCAGGAGTCCATG 552 	음 성
1441	433 TACGGCATCCTCCCGGAGATCATCGGGGACTGCTGCTACGAGGAGTACAAGGACCGCAAG 492	유 성
1381	373 GGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGACGAGCTGGCCTTC 432	B 8
1321	GAG	음 성
1261	253 TACCCCGGACACCCTGCTGGGCAGCACGGAGAAGGAGTTCTTCTTCAACGAGGACACCAAG 312	유
1201	193 CTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACCACGCTGGAGCGC 252	음 성
1141 A	133 CCGGTGGCCAACTGCCCCATGCCCCTGGCCCCGGCCGACAAGAACAAGCGGCAGGATGAG 192	유왕
1153	cnes 1909; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  73 ATGGCGGCCGGAGTTGCGGCCTGGCTGCCTTTTTGCCCCGGGCTGCGGCCATCGGGTGGATG 132	음성 3
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1 (bases 1 to 1968)
Kong, W. and Tomaselli, G.F.
Direct Submission
Submitted (17-FEB-1998) Medicine, Johns Hopkins University of Medicine, 720 Rutland Avenue, Ross 844, Baltimore, MD incation/Qualifiers
                                                                                                                               GGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGACGAGGTGGCCTTC
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Db 241 GAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTTCTACCGCACG 300	ACCCGGACACCCTGCTGGGCAGCACGGAGAAGGAGTTCTTCTTCAACGAGGACAC AGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTTCTACCC	253 TACCCGGACACCCTGCTGGGCAGCACGGAGAAGGAGTTCTTCTAACGAGGACACCAAG 3		QY 133 CCGGTGGCCAACTGCCCCATGCCCCTGGCCCGGCCGACAAGAACAAGCGGCAGGATGAG 192	73 ATGGCGGCCGGAGTTGCGGCCTGGCTGCCTTTTGCCCGGGCTGCGGCCATCGGGTGGATG 13	Query Match Best Local Simila: Matches 1908; Co	/organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644"	PATENT: WO 9842833-A 3 01-OCT-1998; BRIL ANTOINE MICHEL ALAIN (FR); CALMELS THIERRY Location/Qualifiers	unclassified.  1 (bases 1 to 2072)  Bril, A.M. and Calmels, T.P.  KV POTASSIUM CHANNEL POLYPE	nide	A85166 2072 bp DNA linear PAT 21-JAN-200 DEFINITION Sequence 3 from Patent WO9842833.	1921 AAC	3CGCTAACCCCAGAGGGGGAAAGTCGGCCACCCCCTGCCAGCCCAGGCCCAAC ATTCCTTCCATAACCAGCAATGTTGTCAAGGTCTCTGTCTTGTAA 1983 	T CTGAGACCAAAACTGCAAAAACATCCCAGATCACCACAGCCATCATCAGCATCAGCATCAGCATCAGCAGCCAGC	y 1816 CTGAGACCAAACTGCAAAACATCCCAGATCACCACAGCCATCATCAGCATCCCCACTCCC 18	Qy 1756 AGTGAGCAGCCCTCCCTCACAACCAGTCGCTCCAGCCTTAATTTGAAAGCAGACGACGGA 1815		Db 1621 GGCCTGCTACCACCTGCTGCTCCCGTCGTAGTAAGAAGACCACGATCCACACCCCAATTCT 168	Db 1561 ATGGAGAGTTCAATGCAGAACTACCCATCCACAAGAAGTCCCTCACTGTCCAGCCACCCA 162  Qy 1636 GGCCTCACTACCACCTGCTGCTGCTCGTCGTAGTAAGAAGACCACACCACCCCAATTCT 169
321 TACCTGCACAGCAAGCGCAACGGGCTCCTCAACGAGGCGCTGGAGCTGACGAGCCACCACCTCACTCA	1393 TACCTGCACAGCAAGCGCAACGGGGCTCCTCAACGAGGCGCTGGAGCTGACGGGCACCCCA 145	Qy 1333 GCACAAAAGACGCCCCCCTTGCCAGGATCCGTGTGGCCAAAACAGGCAGTTCGAATGCA 1392	1273 GTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAGAGCTGATAAACGCAGG 13 	1213 AAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTTGCTCATTGCCCTGCCAGTCCTT 127	1153 ACCATTGTCACCATGACCACACTGGGATACGAGACATGGTGCCTAAGACGATTGCAGGG 12	1093 TATGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCCTGCCTCGTTTTGGTAC 115	Qy 1033 CTGGGCTTTCTTCTCTTCTCCCTCACCATGGCCATCATCTTTGCCACTGTGATGTTT 1092	Qy 973 TCCCGCCACTCCCAGGGCCTGCGGATCCTGGGCTACACACTGAAGAGCTGTGCCTCCGAA 1032	13 GACGT       41 GACGT	Qy 853 ATCATCGACGTGGTGGCCATCATGCCCTACTACATCGGTCTGGTCATGACCAACAACGAG 912	Qy 793 TACCTCCTGCGGGCTCTTCGCGGCTCCCAGCCGCTTCATCCGCAGCGTCATGAGC 852	Qy 733 CGCTACTCGGTGGCCTTCTTCTGCCTGGACACGGCGTGCGT	O QY 673 GTGGTGGAGAGCGGTGCCGTGCGGCACGGCAAGGAGCTGCCGTGCGGGAG 732	3 CIGGCCCIGGICTICIACIACGIGACIGGCTTCTTCATCGCTGTCTCGGTCATCACCAAC 6/	Db 481 CCCTCGCTCAGCTTCCGCCAGACCATGTGGGGGGCCTTCGAGAACCCCCACAGCAGCAGG 54	Db 421 Adddadadcdccdaddddddddddddddddddddddddd	Qy 493 AGGGAGAACGCCGAGCGGCTCATGGACGACGACGACGAGGAGAACCAAGGAGTCCATG 55	OY 433 TACGGCATCCTCCCGGAGATCATCGGGGACTGCTACGAGGAGTACAAGGACGCAAG 492	O QY 373 GGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGACGACGAGCTGGCCTTC 432

Query Match Best Local Similarity 96.9%; Pred. No. 3.2e-273; Matches 1908; Conservative O; Mismatches 5; Indels 57; Gaps 1;  Qy 73 ATGGCGGCCGGAGTTGCGGCCTGGCTGCTTTTGCCCGGGCTGCGGCCATCGGGTGGATG	NISM ORS E ES Ource	SULT 14 204885 AR204885 CUS AR204885 FINITION Sequence 3 from patent US 6368823. CESSION AR204885 YWORDS URCE Unknown.	1876 CCAGCGCTAACCCCAGAGGGGGAAAGTCGGCCACCCCCTGCCAGCCCAAGGCCCCAACACG	1681 AACCTGCCAGCTACTCGCCTGCGAGCATGCAAGAGCTCAGCATGCACAAGCAGGCC 1  1756 AGTGAGCAGCCCTCCCTCACAACCAGTCGCTCCAGCCTTAATTTGAAAGCAGACGACGACGA 1	QY 1576 ATGGAGGTTCAATGCAGGAGTTTATTGATGAGCAGATGTTTGAGCAGAACTGC 1560 QY 1576 ATGGAGGTTCAATGCAGAACTACCCATCCACAAGAAGTCCCTCACTGTCCAGCCACCCA 1635	
	913 GACGTGTCCGGCGCCTTCGTCACGCTCCGGGTCTTCCAGGATCTTCAAGTTT 972	661 ĠĠĊĪĀĊĪĊĠĠĪĠĠĊĊŦŤĊŤŢĊŢĠĠĊŢĠĠĀĊĀĊĠĠĠŢĠĠŢĊĀŢĠĀŶĊŢŢĊĀĊ	541 CTGGCCTGGTCTTCTACTACGTGA 673 GTGGTGGAGACGGTGCCGTGCGGCA	<b>⊢</b> ∞ ∞ ∞ ∞	241 GAGTACTTCTTCGACCGGGGACCCCCGAGGTGTTCCGCTGCGTGCTCAACTTCTACCGCACG  373 GGGAAGCTGCACTACCCCGCGCTTACGAGTTGCATCCTACGACGACGAGGTGCTTC	93 CTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACCACGCTGGAGCG

ourc	JOURNAL FEATURES	REFERENCE AUTHORS TITLE	SOURCE	DEFINITION ACCESSION VERSION KEYWORDS	RESULT 15 AX956786 LOCUS	Qy da	g Q	g S	d VQ	d VQ	B 8	D Q	Db Qy	g Q	B &	B &	Q Q	Db
.ce 11968 /organism="Homo sapiens" /mol_type="unassigned DNA"	Patent: WO 03097682-A 4 27-NOV-2003; Devgen NV (BE) Location/Qualifiers	1 Kaletta,T.J., Dewulf,N.E. and Plaetinck,G.K. Methods for identifying and developing compounds the voltage-gated potassium channels of the kv4 family	Homo sapiens (human) M Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates: Catarrhini; Hominidae; Homo.	Sequence 4 from Patent W003097682. AX956786 AX956786.1 GI:40785267		1936 AACATTCCTTCCATAACCAGCAATGTTGTCAAGGTCTCTGTTAAAA 1985 	1876 CCAGCGCTAACCCCAGAGGGGGAAAGTCGGCCACCCCCTGCCAGCCCCAGGCCCCAACACG 1935	1816 CTGAGACCAAAACTGCAAAACATCCCAGATCACCACAGCCATCATCAGCATCCCCACTCCC 1875	1756 AGTGAGCAGCCCTCCCCTCACAACCAGTCGCTCCAGCCTTAATTTGAAAGCAGACGACGGA 1815 	1696 AACCTGCCAGCTACTCGCCTGCGCAGCATGCAAGAGCTCAGCACGATCCACATCCAGGGC 1755	1636 GGCCTCACTACCACCTGCTGCTCCCĞTCGTAGTAAĞAAGACCACACCTGCCCAATTCT 1695 	1576 ATGGAGAGTTCAATGCAGAACTACCCATCCACAAGAAGTCCCTCACTGTCCAGCCACCCA 1635	1534AACCACGAGTTTATTGATGAGGAGATGTTTGAGCAGAACTGC 1575	1513 CACTGCCTGGAAAAAACCACT1533 	1453 GAAGAGGAGCACATGGGCAAGACCACCTCACTCATCGAGAGCCAGCATCATCACCTGCTG 1512	1393 TACCTGCACAGCAAGCGCAACGGGCTCCTCAACGAGGCGCTGGAGCTGACGGGCACCCCA 1452	1333 GCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAACAGGCAGTTCGAATGCA 1392	
Qy	D QY	Ωy	D Qy	. Qy	Qy db	Qу	B &	Qy db	D Qy	Qy Bb	B &	D Qy	g Q	B 82	B &	B &	Query Ma Best Loc Matches	ORIGIN
1033 CTGGGCTTTCTTCTCTCTCCCTCACCATGGCCATCATCATCTTTGCCACTGTGATGTTT	973 TCCCGCCACTCCCAGGGCCTGCGGATCCTGGGCTACACACTGAAGAGCTGTGCCTCC	913 GACGTGTCCGGCGCCTTCGTCACGCTCCGGGTCTTCCGCGTCTTCAGGATCTTCAAG	853 ATCATCGACGTGGTGGCCATCATGCCCTACTACATCGGTCTGGTCATGACCAACA	793 TACCTCCTGCGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCATCCGCAGCGTCATGAG	733 CGCTACTCGGTGGCCTTCTTCTGCCTGGACACGGCGTGCGT	673 GTGGTGGAGACGGTGCCGTGCGGCACGGTCCCGGGCAGCAAGGAGCTGCCGTGCGGGGAG	613 CTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTCGGTCATCACCAA	553 CCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGGCCTTCGAGAACCCCCCACACCAGCACG	493 AGGGAGAACGCCGAGCGGCTCATGGACGACAACGACTCGGAGAACAACCAGGAGTCCATG	433 TACGGCATCCTCCCGGAGATCATCGGGGACTGCTGCTACGAGGAGTACAAGGACCGCAAG	373 GGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGACGAGCTGGCCTTI	313 GAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTTCTACCGCAC	253 TACCCGGACACCCTGCTGGGCAGCACGAGAAGGAGTTCTTCTTCAACGAGGAC	193 CTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACCACGC	133 CCGGTGGCCAACTGCCCCATGCCCCTGGCCCCGGCCGACAAGAACAAGCGGCAGGATGAG	73 ATGGCGGCCGGAGTTGCGGCCTGGCTGCCTTTTTGCCCCGGGCTGCGGCCATCGGGT	y Match 89.0%; Score 1836; DB 6; Length 1968 Local Similarity 96.8%; Pred. No. 6.6e-273; nes 1906; Conservative 0; Mismatches 5; Indels 5	/db_xref="taxon:9606"

	AACATTCCTTCCATAACCAGCAATGTTGTCAAGGTCTCTGTCTTGTAA 1983	1936 1921	8 8 9
1920	B61 CCAGCGCTAACCCCAGAGGGGGAAAGTCGGCCACCCCTGCCAGCCCAGGCCCAACACG 192		B 4
	CTGAGACCAAACTGCAAAACATCCCAGATCACCACAGCATCATCATCAGCATCCCCACTCCCCCCCC		S B
	CTGAGACCAAACTGCAAAACATCCCAGATCACCACAGCCATCATCAGCATCCCCACTCCC	1816	i 8
1800	AGTGAGCAGCCCTCCCTCACAACCAGTCGCTCCAGCCTTAATTTGAAAGCAGACGACGAC	1741	뫄
1815	AGTGAGCAGCCTCCCTCACAACCAGTCGCTCCAGCCTTAATTTGAAAGCAGACGACGGA :	1756	8
	AACCTGCCAGCTACTCGCCTGCGCAGCATGCAAGAGCTCAGCACGATCCACATCCAGGGC	1681	Db
1755	AACCTGCCAGCTACTCGCCTGCGCAGCATGCAAGAGCTCAGCACGATCCACATCCAGGGC	1696	Ş
1680	GGCCTCACTACCACCTGCTGCTCCCGTCGTAGTAAGAAGACCACACACCTGCCCAATTCT		밁
1695	GGCCTCACTACCACCTGCTGCTCCCGTCGTAGTAAGAAGACCACACACA		Ş
1620	ATGGAGAGTTCAATGCAGAACTACCCATÇCACAAGAAGTCCCTCACTGTCCAGCCACCCA	1561	Вp
1635	ATGGAGAGTTCAATGCAGAACTACCCATCCACAAGAAGTCCCTCACTGTCCAGCCACCCA		Ş
1560	CGAACCTCCACCATCAAGAACCACGAGTTTATTGATGAGCAGATGTTTGAGCAGAACTGC	1501	Дb
1575	AACCACGAGTTTATTGATGAGCAGATGTTTGAGCAGAACTGC		8
1500			망
1533	CACTGCCTGGAAAAAACCACT	1513	Ş
1440	GAAGAGGAGCACATGGGCAAGACCACCTCATCGAGAGCCAGCATCATCACCTGCTG	1381	망
1512	GAAGAGGAGCACATGGGCAAGACCACCTCACTCATCGAGAGCCAGCATCATCACCTGCTG	1453	Ş
1380	TACCTGCACAGCAACGGCTCCTCAACGAGGCGCTGAACGAGCTGACGGGCACCCCA	1321	망
1452	TACCTGCACAGCAAGCGCAACGGGCTCCTCAACGAGGCGCTGGAGCTGACGGGCACCCCA		Ş
1320	GCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAACAGGCAGTTCGAATGCA	1261	망
1392	GCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAACAGGCAGTTCGAATGCA		S
	GTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAGAGCTGATAAACGCAGG		ర్జ
1332	GTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAGAGCTGATAAACGCAGG		Ş
1200	AAGATCTTCGGCTCCATCTGCTTCAGTGGCGTCCTGGTCATTGCCCTGCCAGTCCCT	1141	皮
1272	AAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCATTGCCCTGCCAGTCCCT		8
1140	ACCATTGTCACCATGACCACACTGGGATACGGAGACATGGTGCCTAAGACGATTGCAGGG	1081	В
1212	ACCATTGTCACCATGACCACACTGGGATACGGAGACATGGTGCCTAAGACGATTGCAGGG :		ঠ
1080	TATGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCCTGCCTCGTTTTGGTAC	1021	ఠ
1152	TATGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCCTGCCTCGTTTTGGTAC		δ
1020	CTGGGCTTTCTTCTCTCTCCCTCACCATGGCCATCATCATCTTTTGCCACTGTGATGTTT	961	Дb

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Abd33130 Human can	13 ABD33130	3004	11.6	240	<b>4</b> .
Ads16307 Rabbit vo	13 ADS16307	2882	12.9	266	44
Adm43511 Human ova	12 ADM43511	3254	15.7	324.6	43
Adj11250 Human ova	12 ADJ11250	3254	15.7	324.6	42
Adm10920 Human O64	11 ADM10920	3254	15.7	324.6	41
Abs24615 Human gen	6 ABS24615	612	16.4	338	40
Abs50654 Human liv	4 ABS50654	612	16.4	. 338	39
Aak25090 Human bra	4 AAK25090	612	16.4	338	38
Aak51097 Human bon	4 AAK51097	612	16.4	338	37
Aba40984 Probe #19	4 ABA40984	612	16.4	338	36
	4 AAI57133	612	16.4	338	IJ U
	4 ABA76453	612	16.4	338	34
Aai28128 Probe #18	4 AAI28128	612	16.4	338	LJ LJ
Adm43516 Human ova	12 ADM43516	1597	17.2	354.4	32
Adj11255 Human ova	12 ADJ11255	1597	17.2	354.4	31
Adm10925 Human O64	11 ADM10925	1597	17.2	354.4	30
Aah21264 Human Kv4	4 AAH21264	1083	17.3	357	29
Adf91396 Worm Kv4.	12 ADF91396	1737	21.4	441.4	28
Abl29810 Drosophil	4 ABL29810	8075	26.2	540	27
Ach91582 Human gen	12 ACH91582	1121	30.7	634.2	c 26
Aah21248 Human KCN	4 AAH21248	2033	30.9	637.8	25
Adm43515 Human ova	12 ADM43515	5404	32.9	679	24
Adj11254 Human ova	12 ADJ11254	5404	32.9	679	23 ·
Adm10924 Human O64	11 ADM10924	5404	32.9	679	22
Abl29811 Drosophil	4 ABL29811	1716	36.1	744.6	21

## ALIGNMENTS

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Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;
nootropic; neuroprotective; cardiant; gene therapy; gene; ss.
                                                                WPI; 2002-556093/59.
P-PSDB; ABB79585.
                                                                                      Cockett MI, Dilks DW,
                                                                                                                   23-OCT-1998;
                                                                                                                                                                                                                                                      Human Kv4.3 potassium channel (short form) cDNA.
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                                                                                                                                                                                                                                                                                   ABN84401;
                                                                                                                                                                                                                                                                                                 ABN84401 standard; cDNA; 2064
                                                                                                                                 23-OCT-1998;
                                                                                                                                                28-MAY-2002
                                                                                                                                                               US6395477-B1.
                                                                                                                                                                                                                  Homo sapiens
                                                                                                    (AMHP ) AMERICAN HOME PROD CORP
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                                                                                                                   98US-00178109.
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                                                                                                                                                                                           Location/Qualifiers
73. .1983
                                                                                                                                                                             /*tag= a
/product= "Kv4.3"
                                                                                                                                                                                      '*tag=
                                                                                      Ling HC,
                                                                                                                                                                                                                                                                                                 BP.
                                                                                      Sokol PT;
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New isolated polynucleotide encoding human Kv4.3 potassium channel polypeptide, useful as probe in a diagnostic method for detecting acid encoding human Kv4.3, and for treating Alzheimer's and heart

nucleic

The present sequence is that of cDNA encoding the short isoform of

novel

Claim 7; Col 21-22; 19pp; English.

diseases.

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                    The present sequence is that of cDNA encoding the long isoform of novel thuman potassium channel Kv4.3. To obtain the cDNA, oligonuclectides based on the published rat sequence were used to screen a whole heart cDNA library. A 511 bp fragment was obtained and used as a probe to rescreen the library. The resulting clones lacked the extreme 5' and 3' coding regions, and 5' and 3' RACE was therefore used to amplify these sequences from a human brainstem cDNA library. 2 Isoforms of human Kv4.3 were identified. One form is full-length (hKv4.3 long) while the second form that a deletion of 19 amino acids in the carboxy domain after the predicted sixth transmembrane domain (hKv4.3 short). Human heart corimarily expresses hKv4.3 long, whereas human brain contains both forms. The invention provides Kv4.3 polypeptides, polynucleotides, and methods for producing these polynucleotides. The Kv4.3 polypeptides and methods corrected the second in the diagnosis, treatment and screening of human diseases relating to an excess or deficiency of hKv4.3 activity, including Alzheimer's disease and heart disease
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nootropic; neuroprotective; cardiant; gene therapy; gene; ss.
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                   AAATCCCGCGGCCATGGCCGGGCCGGGAGCATGCGACGTCGGGCCCAATTCGCCCCTATAGTG
                                                             GGCCCCAACACGAACATTCCTTCCATAACCAGCAATGTTGTCAAGGTCTCTGTCTTGTAA
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                                                                                                                                 ATCCCCACTCCCCAGCGCTAACCCCAGAGGGGGAAAGTCGGCCACCCCTGCCAGCCCA
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AAATCCCGCGGCCATGGCGGCCGGGAGCATGCGACGTCGGGCCCAATTCGCCCTATAGTG
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                                                                                                                                                            This cDNA sequence codes for human Kv potassium channel hKv4.3 (see CC AAW79589). It shows about 92% identity in 1913 nucleotides to rat Kv4.3. CC A1914 bp fragment corresponding to hKv4.3 full-length cDNA was isolated from human heart cDNA by PCR amplification (see AAV61574-77). Another CC claimed polynucleotide (see AAV61572) encodes an isoform (see AAW79599) CC of hKv4.3 having an additional 19 amino acids. The invention relates to these hKv4.3 polynucleotides and polypeptides and to methods for CC producing such polypeptides by recombinant techniques. Also claimed are methods for utilising the hKv4.3 polynucleotides for the treatment of cc subjects in need of enhanced or reduced activity or expression of hKv4.3 CC polypeptide. These include the treatment of cardiac arrhythmias and CC Alzheimer's disease. The invention can also be used to identify agonists CC and antagonists of hKv4.3, and to detect disease associated with CCC inappropriate hKv4.3 expression or activity
Query Match
Best Local Similarity
Matches 1914; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-1997;
09-DEC-1997;
11-DEC-1997;
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P-PSDB; AAW79589.
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09-DEC-1997;
11-DEC-1997;
                                                                                                            WPI; 199
P-PSDB;
                                          New potassium channel polypeptides, hKv4.3 - and hKv4.3-encoding poly:nucleotide(s) useful in the treatment of disorders including cardiac arrhythmias and Alzheimer's disease.
                Claim
                                                                                                                                                                                                                                                                                         23-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV61572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV61572 standard; cDNA;
                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM LAB PHARM.
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DB; AAW79590.
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This cDNA sequence codes for human Kv potassium channel hKv4.3 (see AAW79590). It shows about 92% identity in 1932 nucleotides to rat Kv4.3. A 1914 bp fragment corresponding to hhKv4.3 full-length cDNA was isolated from human heart cDNA by PCR amplification (see AAV61574-77). Another claimed polynucleotide (see AAV61571) encodes an isoform (see AAW79589) of hKv4.3 having 19 fewer amino acid residues. The invention relates to these hKv4.3 polynucleotides and polypeptides and to methods for producing such polypeptides by recombinant techniques. Also claimed are methods for utilising the hKv4.3 polynucleotides for the treatment of subjects in need of enhanced or reduced activity or expression of hKv4.3 polypeptide. These include the treatment of cardiac arrhythmias and Alzheimer's disease. The invention can also be used to identify agonists and antagonists of hKv4.3, and to detect disease associated with inappropriate hKv4.3 expression or activity
2072 BP; 449 A; 681 C; 541 G; 401 T; 0
U; 0 Other;
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89.1%;

Score 1838; Pred. No. 0;

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Length 2072; Indels

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TACCTCCTGCGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCATCCGCAGCGTCATGAGC
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                   The invention relates to a nematode worm that expresses a heterologous nucleotide sequence encoding a functional voltage-gated potassium channel of the Kv4 family, or its analog, mutant, variant, homolog, ortholog, capart or fragment. The nematode worm is useful in determining whether a compound interacts with the voltage-gated potassium channel of the Kv4 capart or whether a compound is an agonist, antagonist, opener and/or blocker of the voltage-gated potassium channel expressed by the nematode worm. The methods are used for identifying and developing compounds that compounds may be used in the development and/or preparation of compounds may be used in the development and/or preparation of these may be used in preparing compositions for pharmaceutical, agrochemical and/or veterinary use. These may be used in preparing compositions for preventing or treating capares or conditions such as arrhythmia, tachycardia, congestive heart failure, epilepsy, stroke, traumatic brain injury, anxiety, insomnia, capareter's disease or arrhythmia, tachycardia, congestive heart strained or preparation of capareter's disease or arrhythmia, tachycardia, congestive heart capareter's disease or arrhythmia arrhythmia archycardia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nematode worm expressing a heterologous nucleotide sequence encoding a functional voltage-gated potassium channel of the Kv4 family, useful for determining compounds that interact with the voltage-gated potassium
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973 TCCCGCCACTCCCAGGGCCTGCGGATCCTGGGCTACACACTGAAGAGCTGTGCCTCCGAA 1032	913 GACGTGTCCGCCCTTCGTCACGCCTTCCGCGTCTTCAGGATCTTCAACGACGACGACGACGACGACGACGACGACGACGACGAC	93 TACCTCCTGCGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCATCCGCAGCGTCATGAGC 85	733 CGCTACTCGGTGGCCTTCTTCTGCCTGGACACGGCGTGCGT	673 GTGGTGGAGACGGTGCCGTGCGGCACGGTCCCGGGCAGCAAGGAGCTGCCGTGCGGGGAG 732	613 CTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTCGGTCATCACCAAC 672	553 CCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGGCCTTCGAGAACCCCCACACCAGCAGC 612	493 AGGGAGAACGCCGAGCGGCTCATGGACGACAACGACTCGGAGAACAACCAGGAGTCCATG 552 	433 TACGGCATCCTCCCGGAGATCATCGGGGACTGCTGCTACGAGGAGTACAAGGACCGCAAG 492	373 GGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGACGAGCTGGCCTTC 432	313 GAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTTCTACCGCACG 372	253 TACCCGGACACCCTGCTGGGCAGCACGGAGAAGGAGTTCTTCTTCAACGAGGACACCAAG 312	TTTCCAGACCTGGAGGACCACGCTGGAGCGC	133 CCGGTGGCCAACTGCCCCATGCCCCTGGCCCCGGCCGACAAGAACAAGCGGCAGGATGAG 192	73 ATGGCGGCCGGAGTTGCGGCTGGCTGCCTTTTGCCCCGGGCTGCGGCCATCGGGTGGATG 132	exy Match 89.0%; Score 1836; DB 12; Length 1968; St Local Similarity 96.8%; Pred. No. 0; Conservative 0; Mismatches 5; Indels 57; Gaps 1;	Sequence 1968 BP; 426 A; 648 C; 511 G; 383 T; 0 U; 0 Other;
RESUL7 AAH21; ID 1 XX XX AC 1 XX	90 92 B	8 B 8	) B 9	P 64	용 &	4g	B &	ob Qy	g dg	р Q	, p 64	B &	ρ <b>δ</b>	4g	, p &	) b
ЛТ 7 21247 AAH21247 standard; cDNA; 2351 вР. AAH21247;	1861 CCAGCGCTAACCCCAGAGGGGAAAGTCGGCCACCCCCTGCCAGCCCAGGCCCAACACG 1920  1936 AACATTCCTTCCATAACCAGCAATGTTGTCAAGGTCTCTGTCTTGTAA 1983	TGAGAC CAAAC TG CAAAACAT CCCAGAT CA CACAGCCAT CAT CAGGCCCAGGCCCCAA 	756 AGTGAGCAGCCCTCCACAACCAGTCGCTCCAGCCTTAATTTGAAAGCAGACGACGGA 181	696 AACCTGCCAGCTACTCGCCTGCGCAGCATGCAAGAGCTCAGCACGATCCACATCCAGGGC 175	636 GGCCTCACTACCACCTGCTGCTCCCGTCGTAGTAAGAAGACCACACACCTGCCCAATTCT 169	5/6 AIGGAGAGTICAAIGCAGAACTACCCAICCACAGAAGICCCICACIGICCAGCCACCCA 163	.534AACCACGAGTTTATTGATGAGCAGATGTTTGAGCAGAACTGC 157	513 CACTGCCTGGAAAAACCACT 153	453 GAAGAGGAGACACISTEGAGACCACCICATICATICAGAGAGCCAGCATICATICATICATICATICATICATICATICATICATI	393 TACCTGCACAGCAAGCGCAACGGCTCCTCAACGAGGCGCTGGAGCTGACGGGCACCCCA 145	333 GCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAACAGGCAGTTCGAATGCA 139	273 GTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAGAGCTGATAAACGCAGG 133	213 AAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCATTGCCCTGCCAGTCCCT 127	153 ACCAITGTCACCAIGACCACACTGGGATACGGAGACAIGGTGCCTAAGACGATTGCAGGG 121	#	961 CTGGGCTTTCTCTCTCTCCCTCACCATGGCCATCATCATCTTTGCCACTGTGATGTTT 1

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Matches 1348
                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel potassium channel protein (I) that is either human Kv4.1 or Kv4.2. Eukaryotic cells that express potassium channels containing (I) are used to identify and test: (i) compounds for treatment of neurodegenerative diseases (autism, epilepsy, ischemia, stroke; Alzheimer's, Parkinson's and Huntington's diseases) or cardiac arrhythmia, or those that improve learning capacity and memory; and (ii) activators of protein kinases. Host cells that express (I) can identify agents that do not interact significantly with channels and control I to (a quickly activated transient current), so lack the side effects of known anti-arrhythmic agents. They also eliminate, or reduce, the need
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Kv4.1; potassium channel protein; Kv4.2; autism; epilepsy; neurodegenerative disease; ischemia; stroke; Alzheimer's disease; Parkinson's disease; Huntington's disease; cardiac arrhythmia; melearning capacity; protein kinase activator; anti-arrhythmic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-426637/46.
P-PSDB; AAB86319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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                                                                                                                                                                                                                                                                                                                                                          Sequence
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14-NOV-2000;
03-APR-2001;
02-OCT-2001;
02-AUG-2002;
              New polynucleotides encoding tumor proteins, treating or inhibiting the development of cancer, particularly ovarian cancer, and for stimulating and/or expanding T cells specific for a tumor protein.
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PS Example 12; SEQ ID NO 253; 221pp; English.

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CC This invention describes a novel ovarian tumour protein which can be used to detecting the presence of an ovarian cancer in a patient by
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This invention describes a novel ovarian tumour protein which can be used to detecting the presence of an ovarian cancer in a patient by stimulating and/or expanding T cells specific for the tumour protein. The products of the invention can also be used in a method to inhibit the development of a cancer in a patient comprising (a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one ovarian tumour protein, such that T cell proliferate and (b) administering to the patient the proliferated T cells. The cytostatic polynucleotides or polypeptides described in the invention are useful for treating or inhibiting the development of cancer, particularly ovarian cancer and for stimulating and/or expanding T cells specific for a tumour protein or for gene therapy.

Sequence 2351 BP; 572 A; 606 C; 591 G; 582 T; 0 U; 0 Other;

Query Match
48.5%; Score 1000.8; DB 11; Length 2351;
Best Local Similarity 72.8%; Pred. No. 1.3e-188;
Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;
Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;

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Query Match Best Local Similarity Matches 1348; Conserv

48.5%; llarity 72.8%; Conservative

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Score 1000.8; DB 12; Pred. No. 1.3e-188; 0; Mismatches 492; I

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Gaps

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GTGGATGCCTGTGGCCTCGGGGCCTATGCCGGCTCCCCCGAGGCAGGAGAGGAAAAGGAC

AGTCACCATGGCGGCGGGGTTGCGGCTGCCTTTTGCCCGGGCTGCGGCCATCGG

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RESULT 9
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01-MAY-2000; 2000US-00561778.
15-AUG-2000; 2000US-00640173.
07-SEP-2000; 2000US-00656668.
14-NOV-2000; 2000US-00713550.
03-APR-2001; 2001US-00825294.
02-OCT-2001; 2001US-00970966.
02-AUG-2002; 2002US-00212677.
05-FEB-2003; 2003US-00361811.
                                                        This invention relates to novel isolated polynucleotides and methods for the therapy and diagnosis of cancer, particularly ovarian cancer. Specifically, it refers to these polynucleotides and the encoded polypeptides thereof, as well as immunogenic peptides, antibodies, antigen presenting cells (APCs) and immune system cells (e.g. T cells) that are targeted to those cells expressing the proteins of interest. The present invention describes methods that are useful for stimulating and/or expanding T cells specific for a tumourigenic protein (i.e. T cell therapy). Furthermore, compositions can be used for the diagnosis, treatment and/or prevention of ovarian cancer by stimulating an immune response in a patient. Accordingly, these compositions exhibit cytostatic activity. This polynucleotide is a human ovarian tumour antigen DNA sequence given in an exemplification of the invention.
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Sequence 2351 BP; 572 A; 606 C; 591 G; 582 T; 0 U; 0 Other;
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01-MAY-2000;
15-AUG-2000;
07-SEP-2000;
14-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel ovarian tumour protein which can be u to detecting the presence of an ovarian cancer in a patient by stimulating and/or expanding T cells specific for the tumour protein. products of the invention can also be used in a method to inhibit the development of a cancer in a patient comprising (a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one ovarian tumour protein, such that T cell proliferate and (b) administering to patient the proliferated T cells. The cytostatic polynucleotides or polypeptides described in the invention are useful for treating or inhibiting the development of cancer, particularly ovarian cancer and stimulating and/or expanding T cells specific for a tumour protein or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides encoding tumor proteins, treating or development of cancer, particularly ovarian cancer, and f and/or expanding T cells specific for a tumor protein.
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02-OCT-2001;
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ic; gene therapy; human;
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07-SEP-2000; 2000US-0065668.
14-NOV-2000; 2000US-00713550.
03-APR-2001; 2001US-00825294.
02-OCT-2001; 2001US-00970966.
02-AUG-2002; 2002US-00212677.
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Best Local Similarity
Matches 1348; Conserv
                                                                                                                                                                                                                                                                                                                                    This invention describes a novel ovarian tumour protein which can be u to detecting the presence of an ovarian cancer in a patient by stimulating and/or expanding T cells specific for the tumour protein. products of the invention can also be used in a method to inhibit the development of a cancer in a patient comprising (a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one ovarian tumour protein, such that T cell proliferate and (b) administering to patient the proliferated T cells. The cytostatic polynucleotides or polypeptides described in the invention are useful for treating or inhibiting the development of cancer, particularly ovarian cancer and stimulating and/or expanding T cells specific for a tumour protein or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding tumor proteins, treating or development of cancer, particularly ovarian cancer, and f and/or expanding T cells specific for a tumor protein.
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Pred. No. 1.5e-188;
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                                       CACGATCCACATCCAGGGCAGTGAGCAGCCCTCCCTCACAACCAGTCGCTCCAGCCTTAA
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Query Match Best Local Similarity

48.5**%**; 72.8**%**;

Score 1000.8; DB 12; Pred. No. 1.5e-188;

5333

BP;

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A; 1136 C;

1167 G;

1520 T; 0

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01-MAY-2000;
15-AUG-2000;
07-SEP-2000;
14-NOV-2000;
03-APR-2001;
02-OCT-2001;
02-AUG-2002;
05-FEB-2003;
                                          This invention relates to novel isolated polynucleotides and methods for the therapy and diagnosis of cancer, particularly ovarian cancer. Specifically, it refers to these polynucleotides and the encoded polypeptides thereof, as well as immunogenic peptides, antibodies, antigen presenting cells (APCs) and immune system cells (e.g. T cells) that are targeted to those cells expressing the proteins of interest. The present invention describes methods that are useful for stimulating and/ or expanding T cells specific for a tumourigenic protein (i.e. T cell therapy). Furthermore, compositions can be used for the diagnosis, treatment and/ or prevention of ovarian cancer by stimulating an immune response in a patient. Accordingly, these compositions exhibit cytostatic activity. This polynucleotide is a human ovarian tumour antigen DNA sequence given in an exemplification of the invention.
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03-APR-2001;
02-OCT-2001;
02-AUG-2002;
05-FEB-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to novel isolated polynucleotides and methods for the therapy and diagnosis of cancer, particularly ovarian cancer. Specifically, it refers to these polynucleotides and the encoded polypeptides thereof, as well as immunogenic peptides, antibodies, antigen presenting cells (APCs) and immune system cells (e.g. T cells) that are targeted to those cells expressing the proteins of interest. The present invention describes methods that are useful for stimulating and/or expanding T cells specific for a tumourigenic protein (i.e. T cell therapy). Furthermore, compositions can be used for the diagnosis, treatment and/or prevention of ovarian cancer by stimulating an immune response in a patient. Accordingly, these compositions exhibit cytostatic activity. This polynucleotide is a human ovarian tumour antigen DNA sequence given in an exemplification of the invention.
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01-MAY-2000;
15-AUG-2000;
07-SEP-2000;
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              GCTGGCCTTCTACGGCATCCTCCCGGAGATCATCGGGGGACTGCTGCTGCTACGAGGAGTACAA
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2000US-00640173.
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              GCACCACCACCTGCTTCACTGCCTGGAAAAAACCACGAATCACGAGTTTGTGGACGAACA
                                                                  GTCCTCAGAGGA----TGAGCAGGCTTTTGTTAGCAAATCCGGCTCCAGCTTTGAAACCCA
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01-MAY-2000; 2000US-00561778.
15-AUG-2000; 2000US-00640173.
07-SEP-2000; 2000US-00656668.
14-NOV-2000; 2000US-00713550.
03-APR-2001; 2001US-00825294.
02-OCT-2001; 2001US-00970966.
                                                                                                The invention relates to an isolated polynucleotide. The invention is used to diagnose, prevent or treat cancer, particularly ovarian cancer. The present sequence represents a human ovarian carcinoma cDNA homologous
                                                                                                                                                                                                              New isolated polynucleotide encoding an ovarian tumor protein for use i diagnosing, preventing or treating cancer, particularly ovarian cancer.
                                          Sequence
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121 A 181 C 241 A 301 G	Query Match Best Local S Matches 2064  1 1 61 121	SULT 1 -09-178-109-3 Sequence 3, Application US/0917810 Patent No. 6395477 GENERAL INFORMATION: APPLICANT: Cockett, Mark I. APPLICANT: Dilks, Daniel W. APPLICANT: Chang Ling, Huai-Ping APPLICANT: Sokol, Patricia T. TITLE OF INVENTION: Human Potassi TITLE OF INVENTION: Polypeptides FILE REFERENCE: ahp-98089 CURRENT APPLICATION NUMBER: US/09 CURRENT FILING DATE: 1998-10-23 NUMBER OF SEQ ID NOS: 4 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 3 LENGTH: 2064 TYPE: DNA ORGANISM: human -09-178-109-3	28 159.8 7.7 8237 4 US-09-949-016-13888 Sequence 29 159 7.7 2084 4 US-09-949-016-3989 Sequence 30 159 7.7 2266 4 US-09-181-339-11 Sequence 31 159 7.7 2266 4 US-09-181-339-11 Sequence 31 159 7.7 2293 3 US-09-336-643A-5 32 159 7.7 19161 4 US-09-949-016-15731 Sequence 33 154.2 7.5 3102 3 US-09-336-643A-17 Sequence 34 150.4 7.1 1805 1 US-09-916-63 35 146.8 7.1 1638 4 US-09-181-339-6 Sequence 36 146 7.1 1638 4 US-09-833-466-2 Sequence 37 146 7.1 2103 4 US-09-833-466-1 Sequence 38 145.6 7.1 248 4 US-09-833-466-1 Sequence 40 143.4 6.9 10304 4 US-09-016-434-790 Sequence 41 141.8 6.9 1518 4 US-09-949-016-16159 Sequence 42 141.2 6.8 17879 4 US-09-949-016-1250 Sequence 43 140 6.8 3186 4 US-09-949-016-1250 Sequence 44 139.6 6.8 6.8 3080 3 US-09-936-643A-7 Sequence 54 136.6 6.6 3080 3 US-09-336-643A-7 Sequence 55 136.6 5.6 3080 3 US-09-336-643A-7 Sequence
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Sequence 1, Application US/09178109
; Patent No. 6395477
; GENERAL INFORMATION:
APPLICANT: Cockett, Mark I.
APPLICANT: Dilks, Daniel W.
APPLICANT: Chang Ling, Huai-Ping
; APPLICANT: Sokol, Patricia T.
TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; TITLE OF INVENTION: Polypeptides and Uses Therefor
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/09/178,109
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2121
; TYPE: DNA
; ORGANISM: human
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RESULT 3 US-09-142 ; Sequence ; Patent 1	B 8	dd VQ	DЪ	Qy dd	D Qy	D Q	Db Qy	Qy dd	d dd	Qy dd	Qy db	D Qy	g Q	B &	gg Qy	g Sy	Qy Db
3 12-791A-1 10ce 1, Application US/09142791A 12 No. 6368823	2044 AGTCGTATTAAAGCCGAATTC 2064                     2101 AGTCGTATTAAAGCCGAATTC 2121	1984 AAATCCCGCGGGCCATGGCGGCCGGGAGCATGCGACGTCGGGCCCAATTCGCCCTATAGTG 2043	1924 GGCCCCAACACGAACATTCCTTCCATAACCAGCAATGTTGTCAAGGTCTCTGTCTTGTAA 1983 	1864 ATCCCCACTCCCCAGCGCTAACCCCAGAGGGGGAAAGTCGGCCACCCCCTGCCAGCCCA 1923	1804 GCAGACGACGGACTGAGACCAAAACTGCAAAACATCCCAGATCACCACAGCCATCATCAGC 1863	1744 CACATCCAGGGCAGTGAGCAGCCCTCCCTCACAACCAGTCGCTCCAGCCTTAATTTGAAA 1803 	1684 CTGCCCAATTCTAACCTGCCAGCTACTCGCCTGCGCAGCATGCAAGAGCTCAGCACGATC 1743	1624 TCCAGCCACCCAGGCCTCACTACCACCTGCTGCTCCCGTCGTAGTAAGAAGACCACACAC 1683	1564 GAGCAGAACTGCATGGAGAGTTCAATGCAGAACTACCCATCCACAAGAAGTCCCTCACTG 1623	15341563	1501 CATCACCTGCTGCACTGCCTGGAAAAAACCACT	1441 ACGGGCACCCCAGAAGAGGAGCACATGGGCAAGACCACCTCACTCA	1381 AGTTCGAATGCATACCTGCACAGCAAGCGCAACGGGCTCCTCAACGAGGCGCTGGAGCTG 1440	1321 GATAAACGCAGGGCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAACAGGC 1380 	1261 CTGCCAGTCCCTGTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAGAGACT 1320	1201 ACGATTGCAGGGAAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCATTGCC 1260	1141 TCGTTTTGGTACACCATTGTCACCATGACCACACTGGGATACGGAGACATGGTGCCTAAG 1200

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GENERAL INFORMATION:

APPLICANT: Antoine Michel Alain Bril
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-François Simon Pierre Faivre
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rouanet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-03-27
PRIOR FILING DATE: 1997-12-09
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
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QY 373 GGGAAGCTGCACTACCGGCGCTACGAGTGCATCTCTGCCTACGACGACGACGAGCTGGCCTTC	Qy 313 GAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTTCTACCGCACG	QY 253 TACCCGGACACCCTGCTGGGCAGCACGGAGAGGAGGTTCTTCTTCAACGAGGACACCAAG	QY 193 CTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACCACGCTGGAGCGCGCGC	QY 133 CCGGTGGCCAACTGCCCCATGCCCCTGGCCCGGCCGACAAGAACAAGCGGCAGGATGAG	Qy 73 ATGGCGGCCGGAGTTGCGGCCTGGCTGTTTGCCCGGGCTGCGGCTGCGTGGATG	Query Match Best Local Si Matches 1909;	LENGTH: TYPE: DN ORGANISM S-09-142-79	PRIOR FILING DATE: 1997-12-11 NUMBER OF SEQ ID NOS: 14 SOFTWARE: FastSEQ for Windows V SEO ID NO 5	PRIOR FILING DATE: 1997-03-27 PRIOR APPLICATION NUMBER: EP 97402971.2 PRIOR FILING DATE: 1997-12-09 PRIOR APPLICATION NUMBER: EP 97403007.4	CURRENT FILING DATE: 1999-02-02 PRIOR APPLICATION NUMBER: PCT/EP98/019 PRIOR FILING DATE: 1998-03-23 PRIOR APPLICATION NUMBER: ITK 9706377	APPLICANT: TITLE OF IN FILE REFERE	APPLICANT: Antoine Michel Alain Bril APPLICANT: Thierry Paul Gerard Calmels APPLICANT: Jean-Francois Simon Pierre Faivre APPLICANT: Jean-Tayre	1 S Or C		Db 1861 ACGAACATTCCTTCCATAGCCAGCAATGTTGTCAAGGTCTCCGCCTTGTAAAACC Qy 1993 GGCCATGGC 2001		Oy 1873 CCCCCAGCGCTAACCCCAGAGGGGGAAAGTCGGCCACCCCCTGCCAGGCCCAGGCCCAAC	QY 1813 GGACTGAGACCAAAACTGCAAAACATCCCAGATCACCACAGCATCAGCATCAGCATCCCCACT
CCTTC 432	372	312	180	192	Oy       Db	Qy Db .	Qy da	Qy dd	Qy da	Qy	Qy	Qy da	Qy Db	Qy Db	1920	1992	1932	1872
1453 GAAGAGGAGCACATGGGCAAGACCACCTCACTCATCGAGAGCCAGCATCATCACCTGCTG 1512	393 TACCTGCACAGCARGCGCAACGGGCTCCTCAACGAGGCGCTGGAGCTGACGGGCACCCCA 145 [	261 GCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAACAGGCAGTTCGAATGCA 132	273 GIGALIGITIC CARCITING COGATTIAC CACAGAAL CAGAGAGAGAGAGAGAGAAACGCAGGATAAACGCAGGATTAACCACCAGAAAACAGAGAGAG	13 AAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCATTGCCCTGCCAGTCCCT 127	153 ACCATTGTCACCATGACCACACTGGGATACGGAGACATGGTGCCTAAGACGATTGCAGGG 12 	093 TATGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCCTGCCTCGTTTTGGTAC 115	TTTGCCACTGTGATGTTT 10                  TTGCCACTGTGATGTTT 10	73 TCCCGCCAC	μω	53 ATCATCGACGT	1	33 CGCTACTCGGTGGCCTTCTTCTGCCTGGACACGG	673 GTGGTGGAGACGGTGCCGTGCGGCACGGTCCCCGGGCAGCAAGGAGCTGCCGTGCGGGGAG 732	13 CTGGCCCTGGTCTTCTACTAC	53 CCCTCGCTCAGCTTCCGCCAGACC		<ul> <li>61 TACGGCÁTCCTCCCGGAGATCATCGGGGACTGCTGCTACGAGGAGTACAAGGACCGC</li> <li>93 AGGGAGAACGCCGAGCGGCTCATGGACGACGACTACGAGTACAACCAGGAGTCC</li> </ul>	01 GGGAAGCTGCACTACACGCGCTACGAGTGCA 33 TACGGCATCCTCCCGGAGATCATCGGGGACT

1153 ACCATTGTCACCATGACCACACTGGGATACGGAGACATGGTGCCTAAGACGATTGCAGGG 12	<u>μ</u>	73 ATGGCGGCCGGAGTTGCGGCCTGGCTGCCTTTTGCCCGGGCTGCGGCCATCGGGTGG	<b>•</b> n
1093 TATGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCCTGCCTCGTTTTGGTAC	Qу в 1: рь	Query Match  89.1%; Score 1838; DB 3; Length 2072; Best Local Similarity 96.9%; Pred. No. 0; Matches 1908; Conservative 0; Mismatches 5; Indels 57	
1033 CTGGGCTTTCTTCTCTCCCTCACCATGGCCATCATCATCTTTTGCCACTGTGATGTTT	. Qу Db	SEQ ID NO 3 TYPE: DIA TYPE: DIA ORGANISM: HOMO SAPIENS 3-09-142-791A-3	us;
973 TCCCGCCACTCCCAGGGCCTGCGGATCCTGGGCTACACACTGAAGAGCTGTGCCTCCGAA	Оу	PRIOR FILING DATE: 1997-12-11 NUMBER OF SEQ ID NOS: 14 SOFTWARE: FastSEQ for Windows Ve	
913 GACGTGTCCGGCGCCTTCGTCACGCTCCGGGGTCTTCCGCGTCTTCAGGATCTTCAAGTTTT	Qy Db	PRIOR FILING DATE: 1997-03-27 PRIOR APPLICATION NUMBER: EP 97402971 PRIOR FILING DATE: 1997-12-09 PRIOR APPLICATION NUMBER: EP 97403007	
853 ATCATCGACGTGGTGGCCATCATGCCCTACTACATCGGTCTGGTCATGACCAACAACGAG	Qy Db	CURRENT FILING DATE: 1999-02-02 PRIOR APPLICATION NUMBER: PCT/EP98/019 PRIOR FILING DATE: 1998-03-23 PRIOR APPLICATION NUMBER: IT 9706377	
793 TACCTCCTGCGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCATCCGCAGCGTCATGAGC	. Qy	APPLIC TITLE FILE I	
733 CGCTACTCGGTGGCCTTCTTCTGCCTGGACACGGCGTGCGT	Qy db	APPLICANT: Antoine Michel Alain Bril APPLICANT: Thierry Paul Gerard Calmels APPLICANT: Jean-Francois Simon Pierre Faivre APPLICANT: Jean-Luc Javre	
21 91 91	Qγ	-09-1 Seque Paten GENER	
613 CTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTCGGTCATCACCAAC	Qγ	3 1921 ACAGÁGĠĠĊ 1929 ESULT 5	RE D
553 CCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGCCTTCGAGAACCCCCACACCAGCACG	1920	1861	δ β
	1992	1933	. <b>.</b>
ACGGCATCCTCCCGGAGATCATCGGGGACTACTGCTGCTACGAGGAGTACAAGGACCGCAA	1932	1873 CCCCCAGCGCTAACCCCCAGAGGGGGAAAGTCGGCCACCCCTGCCAGCCCAGGCCCCAACCCCAACCCCAGCGCCCAACCCCCAGCGCCCAACCCCCAGCGCCCAACCCCCAGCGCCCAACCCCCAGCGCCCAACCCCCAGCGCCCAACCCCCAGCGCCCAACCCCCAGCGCCCAACCCCCAGCGCCAACCCCCAGCGCCCAACCCCCAGCGCCAACCCCCAGCGCCAACCCCCAGCGCCAACCCCAGCGCCAACCCCCAGCGCCAACCCCCAGCGCCAACCCCCAGCGCCAACCCCCAGCGCCAACCCCCAGCGCCAACCCCAGCGCCAACCCCAGCGCCAACCCCCAGCGCCAACCCCCAGCGCCAACCCCCAGCCCCAACCCCCAACCCCCAACCCCCAGCGCCAACCCCCAGCCCCAACCCCCAACCCCCAACCCCAACCCCCAACCCCCAACCCC	5 5
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3 GAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTTCTACC	1680	1621	}
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; Sequence 957, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
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-----CGAACCTCCACCATCAAGAACCACGAGTTTATTGATGAGCAGATGTTTGAGCAGAACTGC
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CATGACCAACGAGGAGGTGTCCGGGGGCCTTCGTCACGCTCCGGGTCTTCCGCGTCTT
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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,49
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Versi
; SEQ ID NO 957
; LENGTH: 5333
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-957
GATCTTCACCGTGGAGTACCTCCTGCGGGCTCTTCGCGGGCTCCCAGCCGCTACCGCTTCAT
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Conservative
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Pred. No. 6.8e-211;
0; Mismatches 492;
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RESULT 7
US-09-336-643A-9
; Sequence 9, Application U
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andre
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APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761el Human Potassium Cha
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 3424
TYPE: DNA
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; FEATURE:
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; LOCATION: (257)...(2195)
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Pred. No. 3.2e-176;
1; Mismatches 559;
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CURRENT APPLICATION NUMBER: US/09/949,016;
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 66.2
Matches 487; Conservative
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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                                         GAATCACGAGTTTGTGGACGAACAAGTCTTTGAAGAAAGCTGCATGGAAGTTGCAACTGT
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Pred. No. 2.4e-62;
0; Mismatches 246;
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 207012
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 2293
LENGTH: 3004
TYPE: DNA
ORGANISM: Human
US-09-949-016-2293
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US-09-949-016-2293
; Sequence 2293, App.
; Patent No. 681233;
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Best Local Similarity 53.4%;
Matches 712; Conservative
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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Pred. No. 2.5e-43;
0; Mismatches 575; Indels 4
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12066
LENGTH: 7055
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; ORGANISM: Human
US-09-949-016-12066
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Patent No. 6812339
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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ACCAACGTGGTGGAGACGGTGCCGTGCGGCACGGTCCCGGGCAGCAAGGAGCTGCCGTGC
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                                                         ATCTCCATTGTCATCTTCTGCCTGGAGACGCTGCCGGAGTTCCGCGACGAGAAGGACTAC
                                                                                    CTGGCCCTGGTCTTCTACTACGTGACTGGCTT-----CTTCATCGCTGTCTCGGTCATC
                                                                                                                                                                 GAGGAGCGGCCCTTGCCCCGCCGCGACTTCCAGCGCCAGGTG---TGGCTGCTCTTCGAG
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Pred. No. 3.2e-43;
D; Mismatches 575; Indels 4
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                                      ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14035
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                                                                                                                                                           FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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Patent No. 6812339
                                                                                                             SOFTWARE: PastSEQ for Windows Version SEQ ID NO 14035
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                NUMBER OF SEQ ID NOS: 207012
                                                                                           LENGTH: 7056
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Best Local Similarity 53.4 Matches 712; Conservative
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; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO 324
; LENGTH: 3004
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-324
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 324, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.3
Matches 710; Conservative
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOMSER: 60/231,498

PRIOR FILING DATE: 2000-09-08

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1604

LENGTH: 1802

TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 565; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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 CGGCGCCTTCGTCACGCTCCCGGGTCTTCCGCGTCTTCAGGATCTTCAAGTTTTCCCGCCA
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                                       CTACGTGAGCCTCACGCTCACGCACCTGGGTGCCCGCATGATGGAGCTGACCAACGTGCA
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                                                                       CTACATCGGTCTGGTCATGACCAACAACGAGG------
                                                                                                              CAAGCTGCACTTCGCGCTGTCCTTCATGAACATTGTGGACGTGCTGGCCATCCTCCCCTT
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                                       US-08-464-340A-3
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Patent No. 5710019
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Potass
NUMBER OF SEQUENCES: 13
 Query Match
                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08449
FILING DATE: 28 JUL 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1744
                                                                                                                               TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2483 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                         TYPE: NUCLEIC
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: June 5,1995
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; STRANDEDNESS:
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PCT-US94-08449A-3
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Best Local Sim
Matches 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2483 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application PC/TUS9408449A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-105
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08449A
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TITLE OF INVENTION: Potassium Channel Protein
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PS/2
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ATTORNEY/AGENT INFORMATION:
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STATE: NEW JERSEY
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Search completed: April 6, 2005, 04:45:42 Job time: 354.233 secs

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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
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Sequence 1, Appli Sequence 3, Appli Sequence 92, Appl Sequence 91, Appl	. 16	Sequence /, Appli Sequence 7, Appli Sequence 7, Appli	3, ,		18,	202	е 9,	95,	e 251,	e 251,	26304, e 251,	Sequence 256, App	e 256,	e 24777	Sequence 255, App	e 255,	e 37	Æ

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## ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/10/062,879
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US/09/178,109
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2064
TYPE: DNA
ORGANISM: human
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US-10-062-879-3
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APPLICANT: Cockett, Mark I.
APPLICANT: Dilks, Daniel W.
APPLICANT: Chang Ling, Huai-Ping
APPLICANT: Sokol, Patricia T.
TITLE OF INVENTION: Human Potassium Channel Polynucleotides
TITLE OF INVENTION: Polypeptides and Uses Therefor
FILE REFERENCE: ahp-98089
                                                                                                                                             Query Match 100.0%; Score 2064; Best Local Similarity 100.0%; Pred. No. 0; Matches 2064; Conservative 0; Mismatches
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1 GATTTGCTGAACTAACTCCAAGCTGGTGTGCCTAGCGTCCGCGGCTGCCGGCCCAAGA
                                                                  GATTTGCTGAACTAACTCCAAGCTGGTGTGCCTAGCGTCCGCCGGCCTGCCCGACCCAAGA
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1021 TGTGCCTCCGAACTGGGCTTTCTTCTTCTTCTCCCTCACCATGGCCATCATCATCATCTTTGCC 1080	61 GCTGGAGTCACATGGCGGCCGGAGTTGCGCCTTGCCTTG
RESULT 2 US-10-062-879-1 ; Sequence 1, Application US/10062879 ; Publication No. US20020127649A1 ; GENERAL INFORMATION: ; APPLICANT: Cockett, Mark I. ; APPLICANT: Dilks, Daniel W. ; APPLICANT: Chang Ling, Huai-Ping ; APPLICANT: Sokol, Patricia T. ; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and ; TITLE OF INVENTION: Polypeptides and Uses Therefor	Oy  1201 ACGASTICCAGGGANAGICTICCACTTCATCTGCTCCTGAGGGCCTCAGGAGAGGAG

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; FILE REFERENCE: ahp-98089
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; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US/09/178,109
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
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                                                   AAGGACCGCAAGAGGGAGAACGCCGAGCGGCTCATGGACGACAACGACTCGGAGAACAAC
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                    TTCACCGTGGAGTACCTCCTGCGGGCTCCTTCGCGGCTCCCAGCCGCTACCGCTTCATCCGC
                                                                                              GTCATCACCAACGTGGAGACGGTGCCGTGCGGCACGGTCCCGGGCAGCAAGGAGCTG
                                                                                                            GTCATCACCAACGTGGTGGAGACGGTGCCGTGCGGCACGGTCCCCGGGCAGCAAGGAGCTG
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE THE TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.484C8
CURRENT APPLICATION NUMBER: US/10/361,811
CURRENT FILING DATE: 2003-02-05
NUMBER OF SEQ ID NOS: 293
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 253
LENGTH: 2351
TYPE: DNA
ORGANISM: Homo sapiens
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Publication No. US20030206918A1
GENERAL INFORMATION:
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Best Local Similarity 72.8%;
Matches 1348; Conservative
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Sequence 253, Application US/10369186

; Publication No. US20030232056A1

; GENERAL INFORMATION:

; APPLICANT: Fanger, Gary R.

; APPLICANT: Fling, Steven P.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.484C9

; CURRENT APPLICATION NUMBER: US/10/369,186

; CURRENT FILING DATE: 2003-02-14

; NUMBER OF SEQ ID NOS: 293

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 253

; LENGTH: 2351

; TYPE: DNA

; ORGANISM: Homo sapiens

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Qy 126 GTGGATGCCGGTGGCCCAACTGCCCCTGGCCCCGCCCGACAAGAACAAGCG 182	Query Match 48.5%; Score 1000.8; DB 15; Length 5333; Best Local Similarity 72.8%; Pred. No. 1.4e-267; Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;  Qy 66 AGTCACCATGGCGGCGGAGTTGCGGTCTGTGTGTTTTGCCGGGCTGCGGCCATCGG 125	; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 252 ; LENGTH: 5333 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-212-677-252	нъхнн		0 01	QY 1857 CATCAGCATCCCCACTCCCCCAGCGCTAACCCCAGAGGGGGAAAGTCGGCCA 1908 	1797 TTTGAAAGCAGACGACGACTGAGACCAAACTGCAAAACATCCCAGATCACCACAGCCAT 185	1737 CACGATCCACATCCAGGGCAGTGAGCAGCCTCCCTCACAACCAGTCGCTCCAGCCTTAA 179 	QY 1677 CACACACCTGCCCAATTCTAACCTGCCAGCTACTCGCCTGCGCAGCATGCAAGAGCTCAG 1736	QY 1617 CTCACTGTCCAGCCACCCAGGCCTCACTACCACCTGCTGCTCCCGTCGTAGTAAGAAGAC 1676	Qy 1557 GATGTTTGAGCAGAACTGCATGGAGAGTTCAATGCAGAACTACCCATCCACAAGAAGTCC 1616	
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Sequence 254, Application US/10212677

Publication No. US20030129192A1

GENERAL INFORMATION:
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APPLICANT: Xu, Jiangchun
APPLICANT: Fanger, Gary R.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Horlocker, Susan L.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C7
CURRENT APPLICATION NUMBER: US/10/212,677
CURRENT FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 288
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 254
LENGTH: 5333
TYPE: DNA
ORGANISM: Homo sapiens
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                    CCAAGATGCTCTCATTGTGCTGAATGTGAGTGGCACCCGCTTCCAGACGTGGCAGGACAC
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                                                                                                                                                                                                                                                                                TGCCACTGTGATGTTTTATGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCC
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                                                             TGCCCTGCCAGTCCCTGTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAG
                                                                                                                              TAAGACGATTGCAGGGAAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCAT 1256
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                                                                                                                                                                                                                                                                                                                                                                                                        CAGGATCTTTAAGTTTTCCCCGCCACTCTCAAGGCCTGCGCATCCTGGGGTACACACTGAA
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Query Match  48.5%; Score 1000.8; DB 17; Length 5333;  Best Local Similarity 72.8%; Pred. No. 1.4e-267;  Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;  Qy  66 AGTCACCATGGCGGGGGGGGGGCTGGCCTTTTGCCCGGGCTGCCATCGG 125	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.484C8 CURRENT APPLICATION NUMBER: US/10/361,811 CURRENT FILING DATE: 2003-02-05 NUMBER OF SEQ ID NOS: 293 SOFTWARE: FAStSEQ for Windows Version 4.0 SEQ ID NO 252 LENGTH: 5333 TYPE: DNA ORGANISM: Homo sapiens US-10-361-811-252	ESULT 8 S-10-361-811-252 Sequence 252, Application US/10361811 Publication No. US20030206918A1 GENERAL INFORMATION: APPLICANT: Fanger, Gary R. APPLICANT: Fling, Steven P.	Qy 1797 TTTGAAAGCAGACGACGACTGAGACCAAACTGCAAAACATCCCAGATCACCACAGCCAT 1856	Qy 1677 CACACACCTGCCCAATTCTAACCTGCCAGCTACTCGCCTGCGCAGCATGCAAGAGCTCAG 1736	2456 AGTCTTTGAAGAAAGCTGCATGGAAGTTGCAACTGTTAATCGTCCTTCAAGTCACAGTCC 2  1617 CTCACTGTCCAGCCACCAGGCCTCACTACCACCTGCTGCTCCCGTCGTAGTAAGAAGAC 1	QY 1497 GCATCACCTGCACTGCACTGCACTGAAAAAACCACTAACCACGAGTTTATTGATGAGCA 1556	QY 1437 GCTGACGGGCACCCCAGAAGAGGAGGAGCACATGGGCAAGACCACCTCACTCA	Oy 1377 AGGCAGTTCGAATGCATACCTGCACAGCAAGCGCAACGGGCTCCTCAACGAGGCGCTGGA 1436 	
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126 GTGGATGCCGGTGGCCAACTGCCCCATGCCCCTGGCCCCGGCCGACAAGAACAAGCG 182	66 AGTCACCATGGCGGCCGGAGTTGCGGCCTGGCTGCCTTTTGCCCGGGCTGCGGCCGGC	Query Match 48.5%; Score 1000.8; DB 17; Length 5333; Best Local Similarity 72.8%; Pred. No. 1.4e-267; Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;	LENGTH: TYPE: DN ORGANISM	2-05 s Version 4.0	COMPOSI AND DI 21.484	o. US20030206918A1 MATION: anger, Gary R. Fling, Steven P.	RESULT 9 US-10-361-811-254 ; Sequence 254, Application US/10361811	QY 1857 CATCAGCATCCCCACTCCCCCAGCGCTAACCCCCAGAGGGGGAAAGTCGGCCA 1908	QY 1797 TTTGAAAGCAGACGACGACTGAGACCAAAACTTGCAAAACATCCCAGATCACCACAGCCAT 1856	Qy       1737       CACGATCCACACCAGGCAGTGAGCAGCCCTCACCAACCAGTCGCTCCAGCCTTAA 1796	QY 1677 CACACACCTGCCCAATTCTAACCTGCCAGCTACTCGCCTGCGCAGCATGCAAGAGCTCAG 1736	QY 1617 CTCACTGTCCAGCCCAGGCCTCACTACCACCTGCTGCTCCCGTCGTAGTAAGAAGAC 1676	QY 1557 GATGTTTGAGCAGAACTGCATGGAGAGTTCAATGCAGTACCATCCAT	QY       1497       GCATCATCACCTGCACTGCACTGGAAAAAACCACCTAACCACGAGTTTATTGATGAGCA 1556	Qy 1437 GCTGACGGGCACCCCAGAAGAGGAGCACATGGGCAAGACCACCTCACTCA	Qy 1377 AGGCAGTTCGAATGCATACCTGCACAGCCAAGCGCAACGGGCTCCTCAACGAGGCGCTGGA 1436	Db 2219 AGCAGACAAAACGAAGGGCACAAAAAGGACTAGACTGGCCAGGATCCGGCCAGAAAC 1376  2219 AGCAGACAAAACGAAGGGCACAAAAGAAAGGCTAGACTGGCCAGGATCCGGGCAGCCAAAAAG 2278	15.1 しょくく はんしつじじゅじゅじしゅんじゅうしゅうしゅうしゅくしゅくしゅくじゅん ないかんじゅん なんしんしゅん しょうしょしゅんしゅんしゅく しょく
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119/ TANGACGATIGCAGGAAGATCTTCGGTTCATCTGCTCCTTGAGTGGGGTCTTGGTCAT 1250	137 TGCCTCGTTTTGGTACACCATTGTCACCATGACCACACTGGGATACGGAGACATGGTGCC 119	1077 TGCCACTGTGATGTTTTATGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCC 1136	1017 GAGCTGTGCCTCCGAACTGGGCTTTCTTCTTCTCCCTCACCATGGCCATCATCATCTT 1076 	957 CAGGATCTTCAAGTTTTCCCGCCACTCCCAGGGCCTGCGGATCCTGGGCTACACACTGAA 1016	9	837 CCGCAGCGTCATGAGCATCATCGACGTGGTGGCCATCATGCCCTACTACATCGGTCTGGT 896 	777 GATCTTCACCGTGGAGTACCTCCTGCGGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCAT 836	717 GCTGCCGTGCGGGGAGCGCTACTCGGTGGCCTTCTTCTGCCTGGACACGGCGTGCGT	660 GGTCATCACCAACGTGGAGACGGTGCCGTGCGGCACGGTCCCGGGCAGCAAGGA 716 	600 CCACACCAGCAGGCTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTC 659	543 GGAGTCCATGCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGCCGCCCTTCGAGAACCC 599	483 GGACCGCAAGAGGGAGAACGCCCGAGCGGCTCATGGACGACAACGACTCGGAGAACAACCA 542 	423 GCTGGCCTTCTACGGCATCCTCCCGGAGATCATCGGGGACTGCTGCTACGAGGAGTACAA 482	363 CTACCGCACGGGGAAGCTGCACTACCCCGCGCTACGAGTGCATCTCTGCCTACGACGACGA 422	303 GGACACCAAGGAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTT 362 	243 GCTGGAGCGCTACCCGGACACCCTGCTGGGCAGCACGGAGAAGGAGTTCTTCTTCAACGA 302	183 GCAGGATGAGCTGAATTGTCCTCAACGTGAGTGGGCAGGAGTTCCAGACTTGGAGGACAC 242	る。これでしている。これでは、これできないできないできない。これでは、これでは、これでは、これでは、これでは、これでは、これでは、これでは、

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US-10-369-186-252  Sequence 252, Application US/10369186  Publication No. US20030232056A1  GENERAL INFORMATION:  APPLICANT: Fling, Steven P.  APPLICANT: Fling, Steven P.  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.484C9 CURRENT APPLICATION NUMBER: US/10/369,186  CURRENT APPLICATION NUMBER: US/10/369,186  CURRENT FILING DATE: 2003-02-14  NUMBER OF SEQ ID NOS: 293  SOFTWARE: FRATSEQ for Windows Version 4.0  SEQ ID NO 252  LENGTH: 5333  TYPE: DNA  ORGANISM: Homo sapiens  US-10-369-186-252  Query Match Best Local Similarity 72.8%; Pred. No. 1.4e-267; Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;  MATCHES 1348; Conservative 0; Mismatches 492; Indels 12; Gaps 4;  MATCHES 1348; PROCCATGGCGGCCGGAGTTGCGCTTGCCTTTTGCCCGGGCTATCGG 125  OY  6 AGTCACCATGGCGGCCGGAGTTGCGGCTGCCTTTTGCAAGGGCATCGG 125  Db 959 AGTAATCATGGCGGCGGGGGTGGCAGCGTGGCTTTTGCAAGGGCAGCGGCTATCGG 1018	2696 TGCCAAAATGGAAGAGGTTAAACTAAACTGCAAAACTGCCAGATCACACAGCCAT 1856  2696 TGCCAAAATGGAAGAGTGTTAAACTAAACTGCAAAACTGCCAGATCCCGCCACTACAGCCAT 1856  1857 CATCAGCATCCCCCACTCCCCCAGCGCTAACCCCCAGAGGGGGAAAGTCCGGCCA 1908	7 CACACACCTGCCCAATTCTAACCTGCCAGCTACTCGCCTGCGAGCATGCAAGAGCTCAG 173	1557 GATGTTTGAGCAGAACTGCATGGAGAGTTCAATGCAGAACTACCCATCCACAAGAAGTCC 1616	1437 GCTGACGGCACCCAGAAGAGGAGCACATGGGCAAGACCACCTCACTCGACGAGAGCCA 1496	257 159 317 219 279
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Query Match 48.5%; Score 1000.8; DB 17; Length 5333; Best Local Similarity 72.8%; Pred. No. 1.4e-267; Matches 1348; Conservative 0; Mismatches 492; Indels 12; Gaps	NUMBER OF SEQ ID NOS: 293 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 254 LENGTH: 5333 TYPE: DNA ORGANISM: Homo sapiens S-10-369-186-254	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.484C9 CURRENT APPLICATION NUMBER: US/10/369,186 CURRENT FILING DATE: 2003-02-14	O. US20030232056A1 WATION: anger, Gary R. Fling, Steven P.	186-254	Qy         1857         CATCAGCATCCCCCACTCCCCCAGCGCGTAACCCCCAGAGGGGGAAAAGTCGGCCA         1908	Qy 1797 TTTGANAGCAGACGACGGACTGAGACCAAACTGCAAAACATCCCAGATCACCACAGCCAT	Qy 1737 CACGATCCACATCCAGGCAGTGAGCAGCCCTCCCTCACAACCAGCCGCCCTCAGCCTTAA	QY 1677 CACACCTGCCCAATTCTAACCTGCCAGCTACTCGCCTGCGCAGCATGCAAGAGCTCAG	Qy 1617 CTCACTGTCCAGCCAGCCCAGGCCTCACTACCACCTGCTGCTGCTCCCGTCGTAGTAAGAAGAC	Qy 1557 GATGTTTGAGCAGAACTGCATGGAGAGTTCAATGCAGAACTACCCATCCACAAGAAGTCC	QY 1497 GCATCATCACCTGCTGCACTGCCTGGAAAAAACCACTAACCACGAGTTTATTGATGAGCA	Qy 1437 GCTGACGGGCACCCCAGAAGAGGAGCACATGGGCAAGACCACCTCACTCA	QY 1377 AGGCAGTTCGAATGCATACCTGCACAGCAAGCGCAACGGGCTCCTCAACGAGGCGCTGGA	QY 1317 AGCTGATAAACGCAGGGCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAAAC	Qy 1257 TGCCCTGCCAGTCCCTGTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAG	Qy 1197 TAAGACGATTGCAGGGAAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTGGTCAT
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.979 CGCTACAGTTATGGTACACCATTGTCACCATGACCACCACGGGATACGGAGACATGGTGCC 119	859 CAGGATCTTTAAGTTTTCCCGCCACTCTCAAGGCCTGCGCATCCTGGGGTACACACTGAA  017 GAGCTGTGCCTCCGAACTGGGCTTTCTTCTCTCTCCCTCACCATGGCCATCATCATCTT	897 C 799 G 957 C	837 739	777 GATCTTCACCGTGGAGTACCTCCTGCGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCAT 8	17 19	660 GGTCATCACCAACGTGGTGGAGACGGTGCCGTGCGGCACGGTCCCGGGCAGCAAGGA 7	600 CCACACCAGCACGCTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTC 6	543 GGAGTCCATGCCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGGCCTTCGAGAACCC 5	483 GGACCGCAAGAGGGAGAACGCCCGAGCGGCTCATGGACGACCAACGACTCCGGAGAACAACCA 5	423 GCTGGCCTTCTACGGCATCCTCCCGGAGATCATCGGGGACTGCTGCTGCGAGGAGTACAA 482 	363 CTACCGCACGGGGAAGCTGCACTACCCGCGCGTACGAGTGCATCTCTGCCTACGACGACGA 4	303 GGACACCAAGGAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTT 3	243 GCTGGAGCGCTACCCGGACACCCTGCTGGGCAGCAGGAGGAGGAGTTCTTCTTCAACGA 3	183 GCAGGATGAGCTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACCAC 2	126 GTGGATGCCGGTGGCCAACTGCCCCATGCCCCTGGCCCCGGCCGACAAGAACAAGCG 1	66 AGTCACCATGGCGGCCGGAGTTGCGGCCTGGCTGCCTTTTGCCCGGGCTGCGGCCATCGG 1

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Sequence 9, Application US/10121746;
Publication No. US20030036648A1
; GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Wang, Jian-Wang
ITILE OF INVENTION: No. US20030036648A1e1 Hun
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/10/121,746
; CURRENT FILING DATE: 2002-04-11
pRIOR APPLICATION NUMBER: US/09/336,643A
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: EARLIER APPLICATION
PRIOR FILING DATE: EARLIER APPLICATION
PRIOR APPLICATION NUMBER: EARLIER APPLICATION
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              FR APPLICATION NUMBER: 6
FOR DATE: 1998-08-07
FOR APPLICATION NUMBER: 6
FOR DATE: 1999-01-19
FOR APPLICATION NUMBER: 6
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; NAME/KEY: CDS
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; OTHER INFORMATION: K+Hnov12
US-10-121-746-9
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ORGANISM: H. sapiens
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PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
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GCTTCATCCGCAGCGTCATGAGCATCATCGACGTGGTGGCCATCATGCCCTACTACATCG
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Pred. No. 8.7e-224;
1; Mismatches 559;
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                           GICGGCCACCCCCTGCCAGCCCAGGC
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                                                                                                  AGATCACCACAGCCATCATCAGCATCCCCACTCCCCAGCGCTAACCCCAGAGGGGGAAA
                                                                                                                                       GCCGCTCCAGCCTCAATGCCAAGCCCCATGACAGCCTTGACCTGAACTGCGACAGCCGGG
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Sequence 373, Application US/10296115
; Deblication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 373
; LENGTH: 2578
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-373
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US-10-296-115-373
; Sequence 373, Application US/10296115
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                                                                                                             ACCAGCACGCTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTCGGTC
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ATCACCAACGTGGTGGAGACGGTGCCGTGCGGCACGGTCCCGGGCAG-----CAAGGAG
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Pred. No. 3.3e-218;
0; Mismatches 575;
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                                                                                      CTTAATTTGAAAGCAG-ACGACGGACTGAGACCAAACTGCAAAAC-CATCCCAGATCACCA
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                                                    CTTCAATGCCAAGCCCCATGACAGCCTTGACCTGAACTGCGACAGCGGGGGACTTCGTGG
                                                                                                                                                                                                        AAGACCACACCTGCCCAATTCTAACCTGCCAGCTACTCGCCTGCGCAGCATGCAAGAG 1731
                                                                                                                                                                                                                                                                                                                                                                  GTGTCTTCCCAGCCAGTGGGACCCCGGAAGCCTGCTGTCTTCTTGCTGCCCTCGCAGGGCC
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Sequence 255, Application US/10212677

Publication No. US20030129192A1

GENERAL INFORMATION:
APPLICANT: Chenault, Ruth A.
APPLICANT: Chenault, Ruth A.
APPLICANT: W. Jiangchun
APPLICANT: Fanger, Gary R.
APPLICANT: Harlocker, Susan L.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REPERENCE: 210121.484C7
CURRENT APPLICATION NUMBER: US/10/212,677
CURRENT FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 288
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 255
LENGTH: 5404
TYPE: DNA
ORGANISM: Homo sapiens
US-10-212-677-255
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Best Local Similarity 77.0
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CCACACCAGCACGCTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTTCATCGCTGTCTC
                                                   GAGAGCGCCTTGCCCACCATGACTGCAAGGCAGAGGGTCTGGAGGGCCTTCGAGAACCC
                                                                                                                                  GGACCGCAAGAGGGAGAACGCCGAGGGGCTCATGGACGACAACGACTCGGAGAACAACCA
                                                                                                                                                                                                    GCTGGCCTTCTACGGCATCCTCCCGGAGATCATCGGGGACTGCTGCTACGAGGAGTACAA
                                                                                                                                                                                                                                                                   CTACCGCACGGGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGACGA
                                                                                                                                                                                                                                                                                                                                   GGACACCAAGGAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTT
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                                                                                GGAG---TCCATGCCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGGCCTTCGAGAACCC
                                                                                                                  GGATCGCAGGCGAGAGAACGCCGAGCGCCTGCAGGACGACGCGGATACCGACACCGCTGG
                                                                                                                                                                                  ACTGGCCTTCTTTGGCCTCATCCCGGAAATCATCGGCGACTGCTGTTATGAGGAGTACAA
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77.0%;
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Pred. No. 4.6e-178;
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APPLICANT: Fanger, Gary R.

APPLICANT: Fling, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.484CB;
CURRENT APPLICATION NUMBER: US/10/361,811
CURRENT FILING DATE: 2003-02-05
NUMBER OF SEQ ID NOS: 293
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 255
LENGTH: 5404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-10-361-811-255
; Sequence 255, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-361-811-255
                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 868; Conserva
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Pred. No. 4.6e-178;
0; Mismatches 250; Indels
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AK03268 Mus muscu

AY406812 Homo sapi

AY406814 Mus muscu

AY408063 Homo sapi

AY4080613 Pan trogl

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AL327691 Tetraodon

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## ALIGNMENTS

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O Z	/gene="KCND3" /locus +ac="HCN6847"	gene
0	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"	
<b>3 2</b>		sour
3 Z	Location/Qualifiers	FEATURES
<u> </u>	These sequences were made by sequencing them based on alignment	COMMENT
<b>3 2</b>	Rockville, MD 20850, USA	
3 2	Submitted (16-NOV-2003) Celera Genomics,	JOURNAL
ž Ž	Adams, M.D. and Cargill, M.	
Ž Ž	<pre>Ferriera.S Wang.G Zheng.X.H White.T</pre>	
Ž Ž	Clark, A.G., Glanowski, S., Nielson, R., Tho	AUTHORS
3 Z	to 1911)	REFERENCE
3 2	14671302	PUBMED
Z Ž	gene trios	TANGITOT
3 2	Inferring nonneutral evolution from human	TITLE
3 2	Ferriera, S., Wang, G., Zheng, X.H., White,	
3 2	Todd.M.A., Tanenbaum,D.M., Civello,D.R.,	POTTIONS
3 2	Clark N G Clarowski S Nielson B Th	REFERENCE
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Pan troglodytes KCND3 gene, Vi
genomic survey sequence.
AY419308
AY419308.1 GI:39775265
GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (bases 1 to 1911)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferritera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
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, B		COMMENT FEATURES SOURC	JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL	ORGANISM REFERENCE AUTHORS	RESULT 3 AY419309 LOCUS DEFINITION ACCESSION VERSION KEYMORDS SOURCE	
1 ATGCCGCAAGAGTTGCAGCCTGCCCCATGCCCCTGGCCCGGCCGG	ch al simila 1744; Co	Rockville, MD 20850, USA These sequences were made by sequencing genomic exons and ordering them based on alignment. Location/Qualifiers  1. 1911 ce /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090"	AL Science 302 (5652), 1960-1963 (2003)  ED 14671302  CE 2 (bases 1 to 1911)  RS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  Direct Submission  AL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,	M Mus musculus (Mode Mode)  Mus musculus (Mode)  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  1 (bases 1 to 1911)  Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  Adams, M.D. and Cargill, M.  Inferring nonneutral evolution from human-chimp-mouse orthologous  gene trios	AY419309 Mus musculus KCND3 gene, genomic survey sequence. AY419309 AY419309.1 GI:39775266 GSS.	1873 CCCCCAGCGCTAACCCCAGAGGGGAAAGTCGGCCACCCCCTGCCAGCCCAGGCCCAAC 1932
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213 AAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCTTGGTCATTGCCCTGCCAGTCCCT 12	CTGGGCTTTCTTCTCTCCCCTTACCATGGCCATCATCATCTTTGCCACTGTGATGTTT 102  TATGCCGAGAAGGCTCCTCGGCCAGCAAGTTCACAAGCATCCTTGCCACTGTGATGTTT 102  TATGCCGAGAAGGCTCCTCGGCCAGCAAGTTCACAAGCATCCCTGCCTCGTTTTTGGTAC 115  TATGCTGAGAAGGGCTCCTCTGCCAGCAAGTTCACAAGCATCCCTGCATCTTTCTGGTAC 108  TATGCTGAGAAGGGCTCCTCTGCCAGCAAGTTCACAAGACATCCCTGCATCTTTCTGGTAC 108  ACCATTGTCACCATGACCACACTGGGATACGGAGACATGGTGCCTAAGACGACTATGCAGGG 121	FICCGGCGCCTTCGTCACGCTCCGGGTCTTCCACGATCTTCAAGTT	93 TACCTCCTGCGGCTCTTCGCGGCTCCCAGCCGCTACCGCTTCATCCGCAGCGTCATGAGC 85	41 CIGGCACTGGTCTTCTACTATGTGACTGGCTTCTTCATTGCCGTCTCGGTCATCACCAAT 6 41 CIGGCACTGGTCTTCTACTATGTGACTGGCTTCTTCATTGCCGTCTCGGTCATCACCAAT 6 73 GTGGTGGAGACGGTGCCGTGCGGCACCGGTCCCGGGGAGCTGCCGTGCGGGGAG 7	AGGGAG	373 GGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGACGAGCTGGCCTTC 432

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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AK033962 3730 bp mRNA linear HTC 03-APR-200. Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330129C02 product:potassium voltage-gated channel, Shal-related family, member 3, full insert sequence.
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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6 (bases 1 to 3730)
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URL:http://fantom.gsc.riken.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepare mouse tissues.
Please visit our web site for further details.
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mol_type="mRNA"

strain="C57BL/6J"
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RS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Ri Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed t ď

/tissue\_type="diencephalon"
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/proteIn id="BAC28529.1"
/db xref="GI:26329581"
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PSLSFRQTMWRAPENPHTSTLALVFYYVTGFFIAVSVITNVVETVPCGTVPGSKELPC
GERYSVAPFCLDTACVMIFTVEYLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVM
TNNEDVSGAFVTLRVFRVFRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIII
FATVMFYAEKGSSASKFTSIPASFWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGV
LVIALPVPVIVSNFSRIYHQNQRADKRRAQKKARLARIRVAKTGSSNAYLHSKRNGLL
NEALELTGTPEEEQMGKTTSLIESQHHHLLHCLEKTTVSSSLLPPPASSLTSQGCTHV /note="unnamed protein product; potassium voltage-gated channel, Shal-related family, member 3 (MGD|MGI:1928743, GB|NM\_019931, evidence: BLASTN, 100%, match=1462)

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enriched library, clone:6430513P12 product
mRNA, full insert sequence.
AK032268
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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20499374
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
                                                                                                                  Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new common result.
                                                                                                                                                                                                           Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999) 99279253
                                                                                                                                                                                                                                                                                       Eukaryota;
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

AL Nature 420, 563-573 (2002)

E 6 (bases 1 to 2997)

RS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Youda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,A., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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VRVSAL"
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707 GCAGCAAGGAGCTGCCGTGCGGGACACCGCTACTCGGTGGCCTTCTTCTGCCTGGACA 76	Ş
Db 1562 TCATTGCCGTCTCAGTCATCGCGAATGTGGTGGAAACAGTTCCATGTGGGTCTAGCCCAG 1621	đđ
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CTCAGGACGCTCTGATAGTGCTGAACGTGA	멅
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Query Match 47.8%; Score 985.6; DB 3; Length 2997; Best Local Similarity 72.0%; Pred. No. 8.7e-218; Matches 1343; Conservative 0; Mismatches 509; Indels 12; Gaps 4;	

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ACCESSION
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Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1893)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky; J.J.,

Inferring nonneutral evolution from human-chimp-mouse orthologous
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
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Science 302 (5652), 1960-1963
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                                                                                                      GAGCAGAACTGCATGGAGAGTTCAATGCAGAACTACCCATCCACAAGAAGTCCCTCACTG
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse ortho
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Rockville, MD 20850, USA
This sequence was made by seque
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
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Science 302 (5652), 1960-1963
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                GAGCTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACCACGCTGGAG
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                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                      /gene="KCND2"
/locus_tag="HCM2682"
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                  1 (bases 1 to 1944)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Science 302 (5652), 1960-1963
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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QY 898 ATGACCAACAACGAGGACGTCTCCGGCGCCTTCGTCACGCTCTCCGCGGTCTTCCGCGTCTTC 957	838 CGCAGCGTCATGAGCATCATCGACGTGGTGGTGGCCATCATGCCCTACATCGGTCTGGTC		QY 718 CTGCCGTGCGGGGAGCGCTACTCCGGTGGCCTTCTTCTGCCTGGACACGGCGTGCGT	QY 664 ATCACCAACGTGGTGGAGACGGTGCCGTGCGGCACGGTCCCGGGCAGCAAGGAG 717	OY 604 ACCAGCACGCTGGCCCTGGTCTTCTACTACGTGACTGGCTTCTCATCGCTGTCTCGGTC 663	QY 553 CCCTCGCTCAGCTTCCGCCAGACCATGTGGCGGGCCTTCGAGAACCCCCAC 603	QY 493 AGGGAGAACGCCGAGCGGCTCATGGACGACGACTCGGAGAACAACCAGGAGTCCATG 552	Qy 433 TACGGCATCCTCCCGGAGATCATCGGGGGACTGCTGCTACGAGGAGTACAAGGACCGCAAG 492	OY 373 GGGAAGCTGCACTACCCGCGCTACGAGTGCATCTCTGCCTACGACGAGCTGGCCTTC 432	OY 313 GAGTACTTCTTCGACCGGGACCCCGAGGTGTTCCGCTGCGTGCTCAACTTCTACCGCACG 372	QY 253 TACCCGGACACCCTGCTGGGCAGCACGGAGAAGGAGTTCTTCTTCAACGAGGACACCAAG 312	QY 193 CTGATTGTCCTCAACGTGAGTGGGCGGAGGTTCCAGACCTGGAGGACCACGCTGGAGCCC 252	QY       133       CCGGTGGCCCAACTGCCCCCATGCCCCTGGCCCCGGCCGACAAGAACAAGCGGCAGGATGAG       192	Qy 73 AIGGCGGCCGGAGTIGCGGCCIGGCCIGCCGGCTGCGGCGGCCAICGGGTGGAIG 132	Query Match 40.8%; Score 842; DB 9; Length 1944; Best Local Similarity 68.4%; Pred. No. 1.8e-184; Matches 1284; Conservative 0; Mismatches 555; Indels 39; Gaps 7;	gene <1 >1944 /gene="KCND1" /locus_tag="HCM3099"	source 11944 /organism="Homo sapiens" /mol_type="genomic DNA" /db xref="taxon:9606"
RESULT 9 AY408065 LOCUS AY408065 DEFINITION Mus musculus KCND1 gene, VIRTUAL TRANSCRIPT, partial sequence,	Qy 1909 CCCCTGCCAGCC 1926 	Db 1786 GCTGCCATTATCAGCATCCCCTACCCTGCCAACACCCCAGAGGGGGAAAGTCGGCCA 1908	1789 AGCCTCAATGCCAAGCCCCATGACCAGCCTTGACCTGAACTGCACAGCCGGGACTTCGTG 178	1/29 GAGCICAGACGATCCACAICCAGGGCAGGCCAGCCCTCAGCACCAGCCCTCCC 1 1672 GAGCTGGGCAGGGCCAGGGCCAGGGCCCTCAGAGCCGCTCC 1 1672 GAGCTGGGCAGGGGCGAGGGCCATGCCCCTCAGAGCCGCTCC 1	1672 AAGACCACACCTGCCCAATTCTAACCTGCCAGCTACTCGCCTGCGCAGCATGCAA		1998 AIGITI GAGCAGAACIGCAIGAGAGIICAAIGCAGAACIACCAICACAGAACITCACAGAACITCAAIGCAGAGCAGCAGCAGCAGCAGCAGCACCTCT 1 1492 ACCTTCAGTGAAGCCCTGGGGAGCCGTCTCGCCGGGTGGCCGCACCAGCCGTAGCACCTCT 1	1498 CATCATCACCTGCACTGCACTGCACTGAAAAACCACTAACCACGAGTTTATTGATGAGCAG 1	1438 CTGACGGCACCCCAGAAGAGGAGCACATGGGCAAGACCACCTCACTCA	1378 GGCAGTTCGAATGCATACCTGCACAGCGCAACGGGCTCCTCAACGAGGCGCTGGAG 1	1318 GCTGATAAACGCAGGCACAAAAGAAGGCCCGCCTTGCCAGGATCCGTGTGGCCAAAACA	1258 GCCCTGCCAGTCCCTGTGATTGTTTCCAACTTTAGCCGGATTTACCACCAGAATCAGAGA	1198 AAGACGATTGCAGGGAAGATCTTCGGCTCCATCTGCTCCTTGAGTGGCGTCCATT 1	1138 GCCTCTTTTGGTACACCATTGTCACCACCACCACCAGAGACATACGAGACATAGGTGCCC 1 1081 GCGGCCTTCTGGTATACCATTGTCACCATGACCACGCTTGGCTACGAGACATGGTGCCC 1	1078 GCCACTGTGATGTTTTATGCCGAGAAGGGCTCCTCGGCCAGCAAGTTCACAAGCATCCCT	Qy 1018 AGCTGTGCCTCCGAACTGGGCTTTCTTCTCTCTCTCCCTCACCATGGCCATCATCATCTTT 1077	Qy 958 AGGATCTTCAAGTTTTCCCGCCACTCCCAGGGCCTGCGGATCCTGGGCTACACACTGAAG 1017

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1 (bases 1 to 1956)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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Submitted (16-NOV-2003) Celera
Rockville, MD 20850, USA
This sequence was made by seque
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Location/Qualifiers
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Db	γQ	4g VQ	Best Loo Matches	ORIGIN Query M	Series	3 OF 10	FEATURES	COMMENT	TITLE	PUBMED REFERENCE AUTHORS	TITLE JOURNAL		REFERENCE AUTHORS		SOURCE	VERSION KEYWORDS		AY406813 LOCUS	RESULT 10	מס		Qy	Db X		Qy	Db
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2 (bases 1 to 1939)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
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Science 302 (5652), 1960-1963 (2003)
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Pan troglodytes KCND1 gene, VIRTUAL
genomic survey sequence.
AY408064
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/locus_tag="HCM3099"
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Osato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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Mus musculus adult male epididymis cDNA, RIKEN full-length enriched library, clone:9230112B12 product:potassium voltage-gated channel, Shal-related family, member 1, full insert sequence.
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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                                                                                                                  GTCCGGCGCCTTCGTCACGCTCCCGGGTCTTCCGCGTCTTCAGGATCTTCAAGTTTTTCCCG
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                       GCACTCGCAGGGCCTGAGGATTCTGGGCTACACCCTCAAGAGCTGTGCCTCTGAGCTAGG
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HHLLHCLEKTTCHEFTDELTFSEALGAVSLGGRTSRTSVSSQPMGPGSLFSSCCSRR
VNRRAIRLANSTASVSRGSMQELDTLAGLRRSPAPQTRSSLNAKPHDSLDLNCDSRDF
VAAIISIPTPPANTFDESQPSSPSGGGGSGGTPNTTLRNSSLGTPCLLPETVKISSL"
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channel, Shal-related family, member 1 (MGD|MGI:96671,
GB|NM_008423, evidence: BLASTN, 100%, match=1524)
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/dev_stage="adult"
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BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
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Estimate of human gene number provided by genome using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                  Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F. Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Pred. No. 1.1e-114;
4; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope - Centre National de Sequencage - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
(http://www.chori.org/bacpac/rat230.htm). please contact Pieter de Jong (pdejong@mail.cho.org).
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 390 row: G column: 12
Seg primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Riggs,F., de Jong,P. and Fraser,C.M. Rat BAC End Sequences from Library CHORI-230 Unpublished (1999) Other_GSSs: CH230-390G12.TJ
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CH230-390G12.TV CHORI-230 Segment
CH230-390G12, genomic survey seque
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Mammalia; Eutheria;
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 GACGACAACGACTCGGAGAACAACCAGGAGTCCATGCCCTCGCTCAGCTTCCGCCAGACC
                                  GGCGACTGCTGTGAGGAGTACAA-TACCGCAAGCGGGAGAACGCTGAGCGGCTCATG
                                                                 GATTTTCAAGTTCTCCAGGCACTCGGCGGSGC
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                                                                                                       Conservative
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                                                                                                                                                                                        /cell type="Brain"
/clone lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: Mt
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced
Pieter de Jong"
                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                             /clone="CH230-390G12"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                 organism="Rattus norvegicus"
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Search completed: April 5, 2005, 18:33:27 Job time : 6059.92 secs

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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2 6/ptodata/1/iaa/5A COMB.pep:*

2: /cgn2-6/ptodata/1/iaa/5B COMB.pep:*

3: /cgn2-6/ptodata/1/iaa/6A COMB.pep:*

4: /cgn2-6/ptodata/1/iaa/6B COMB.pep:*

5: /cgn2-6/ptodata/1/iaa/PCTUS COMB.pep:*

6: /cgn2-6/ptodata/1/iaa/backfiles1.pep:*
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APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Faivre
APPLICANT: Jean-Luc Javre
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rouanet
FITTLE OF INVENTION: NOWEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR APPLICATION NUMBER: UX 9706377.0
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Sequence 4, Application US/09178109

; Patent No. 6395477

; GENERAL INFORMATION:

APPLICANT: Cockett, Mark I.

APPLICANT: Dilks, Daniel W.

APPLICANT: Chang Ling, Huai-Ping

; APPLICANT: Schol, Patricia T.

TITLE OF INVENTION: Human Potassium Channel Polynucleotides and

; TITLE OF INVENTION: Polypeptides and Uses Therefor

; FILE REFERENCE: ahp-98089

; CURRENT APPLICATION NUMBER: US/09/178,109

; CURRENT FILING DATE: 1998-10-23

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 4

; LENGTH: 636

TYPE: PRT

; ORGANISM: human
                                                                                                                                                                                                                                                                                                                                YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF 120
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                                                                            YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF
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                       YLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGAFVTLRVFRVFRIFKF
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Pred. No. 1.1e-307;
0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR FILING DATE: 1998-03-23
PRIOR FILING DATE: 1997-03-27
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
PRIOR FILING DATE: 1997-12-09
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
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; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-142-791A-2
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US-09-142-791A-2
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Best Local Similarity
Matches 634; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09142791A Patent No. 6368823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Antoine Michel Alain Bril
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Faivre
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rouanet
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TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
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                                                                                                                                  YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF
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                                                                                                                                                                                                                                            Score 3291.5; DB 3; Pred. No. 7.9e-307; 0; Mismatches 2;
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GENERAL INFORMATION:
APPLICANT: Antoine Michel Alain Bril
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Faivre
APPLICANT: Jean-Francois Simon Pierre Faivre
APPLICANT: Sabine Rouanet
ITILE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02
PRIOR FILING DATE: 1999-03-03
PRIOR FILING DATE: 1997-03-23
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 636
TYPE: PRT
ORGANISM: HOMO SAPIENS
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Matches 630
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630; Conserv
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                                                                 MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKRQDBLIVLNVSGRRFQTWRTTLER
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YPDTILGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF 120
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ilarity 96.2%;
Conservative
                                                                                                            Score 3265.5; DB 3; Pred. No. 2.5e-304; 1; Mismatches 5; 1
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Sequence 6828, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSITITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6828

LENGTH: 630
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US-09-949-016-6828
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                                                                                                          Query Match
Best Local Similarity
Matches 486; Conserv
                                                                                                                                                               TYPE: PRT
ORGANISM: Human
-09-949-016-6828
                                                                                                                                                                                                        LENGTH: 630
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                                                                                                          Conservative
                                                                                                        73.2%; Score 2498.5; DB 4; Length 73.6%; Pred. No. 1.1e-230; Live 69; Mismatches 70; Indels
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OF DETECTION
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APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761el Human Potassium Cha
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR APPLICATION NUMBER: DCT/US99/03826
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
                                                     ; LOCATION: (1)...(646); OTHER INFORMATION: Xaa US-09-336-643A-10
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US-09-336-643A-10
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                                                                                                                                                           NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID 10
Query Match 61.6%;
Best Local Similarity 63.3%;
Matches 428; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                          TYPE: PRT
ORGANISM: H. sapiens
FEATURE:
                                                                                              NAME/KEY: VARIANT
                                                                                                                                                    LENGTH:
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                                                                    Any
  78;
                                                                    Amino
Score 2102; DB 3;
Pred. No. 1.3e-192;
'8; Mismatches 116;
                                                                    Acid
                         Length 646;
  Indels
  54;
  Gaps
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US-09-949-016-8327

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PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8327

LENGTH: 260

TYPE: PRT
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US-09-949-016-8327
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                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                              Sequence 8327, Application US/09949016 Patent No. 6812339
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQHHHLLHCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMFEQNCMESSMQNYPSTRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSVSSQPVGPGSLLSSCCPRRAKRRAIRLANSTASVSR-GSMQELDM--LAGLRRSHAPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGILPEIIGDCCYEEYKDRKRENAERLMDDNDSENNQESMPSL----SFRQTMWRAFENP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQHHHLLHCLEKTT--------CHEFTDELTFSE-ALGAVSPGGRTSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RADKRRAQKKARLARIRVAKTGSSNAYLHSKRNGLLNEALELTGTPEEEHM-GKTTSLIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTSTLALVFYYVTGFFIAVSVITNVVETVPC--GTVPGSKELPCGERYSVAFFCLDTACV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YPDTLLGSSEKEFFYDADSGEYFFDRDPDMFRHVLNFYRTGRLHCPRQECIQAFDEELAF
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APPLICANT: Jegla, Timothy James
APPLICANT: Jegla, Timothy James
APPLICANT: ICAgen, Inc.
TITLE OF INVENTION: Kv10.1, a No. 6727353el
TITLE OF INVENTION: Human Brain
FILE REFERENCE: 018512-005910US
CURRENT APPLICATION NUMBER: US/09/833,466
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/197,793
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-833-466-13; Sequence 13, Application US/09833466; Patent No. 6727353; GEMERAL INFORMATION:
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OTHER INFORMATION: human voltage-gated potassium US-09-833-466-13
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Best Local Similarity
Matches 223; Conser
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Best Local Similarity
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TYPE: PRT
ORGANISM: Homo sapiens
                    240
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EYLLRLFAAPSRYRPIRSVMSIIDVVAIMPYYIGLVMTNN------
                                                                                                                                                         EEYKDRK-----RENAERIMDDNDSENNQESMPSLSFRQTMWRAFENPHTSTLALVFY 186
                                                                                                                                                                                             DYNLNENEYFFDRHPGAFTSILNFYRTGKLHMMEEMCALSFGQELDYWGIDEIYLESCCQ 138
                                                                                                                                                                                                                 -FNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAFYGILPBIIGDCCY 133
                                                                                                                                                                                                                                                                    LPPEPVDIIRSKTCSRRVKINVGGLNHEVLWR-TLDRLPRTRLGKLRDCNTHESLLEVCD
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                                                                                                                         ARYHOKKEOMNEELRREAETMRDGEGEEFDNTCCPDK--RKKLWDLLEKPNSSVAAKILA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYVTTAIISIPTPPVTTPEGDDRPESPEYSGG-----NIVRVSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRRHKKTFRIPNANVSGSHQGSIQELSTIQIRCVERTPLSNSRSSLNAKMEECVKLNCEQ
                                                      IVSILFIVLSTIALSLNTLPELQETDEFGQLNDNRQLA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQITTAIISIPTPPALTPEGESRP--PPASPGPNTNIPSITSNVVKVSVL
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                                                                                      YVTGFFIAVSVITNVVETVP------CGTVPGSKELPCGERYSVAFFCLDTACVMIFTV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------NHEFVDEQVFEESCMEVATVNRPSSHSPSLSSQQGVTSTCC
                                                                                                                                                                                                                                                                                                                                     22.5%; ilarity 27.5%; Conservative 11
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                                                                                                                                                                                                                                                                                                                                         115;
                                                                                                                                                                                                                                                                                                                                     Score 767; DB 4; I
Pred. No. 2.7e-64;
15; Mismatches 243;
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                 -EDVSGAFVTLRVF
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RESULT 10
US-09-833-466-12
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APPLICANT: ICAgen, Inc.
TITLE OF INVENTION: Kv10.1, a No. 6727353el Voltage-Gated Potassium Channel
TITLE OF INVENTION: Human Brain
FILE REFERENCE: 018512-005910US
CURRENT APPLICATION NUMBER: US/09/833,466
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/197,793
PRIOR APPLICATION NUMBER: US 60/197,793
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 854
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application Patent No. 6727353 GENERAL INFORMATION:
                                                                                                                                        Matches
                                                                                                                                                                              Query Match
                                                                                                                                                                                                                               ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human voltage-gated potassium channel
                                                                                                                                                           Local Similarity
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                    75
                                                                                 MPLAPAD--KNKRQDELIVLNVSGRRFQT-WRTTLERYPDTLLG-----STEKEFF----
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-FNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAFYGILPEIIGDCCY
                                                           LPPEPMEIVRSKACSRRVRLNVGGLAHEVLWR-TLDRLPRTRLGKLRDCNTHDSLLEVCD
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                                                                                                                                      21.8%;
ilarity 29.1%;
Conservative 11
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                                                                                                                                     %; Score 742.5; DB 4;
%; Pred. No. 6.7e-62;
116; Mismatches 213;
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                                                                                                                                        213;
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                                                                                                                                        Indels
                                                                                                                                                                          Length
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                                                                                                                                APPLICANT: The Rockefeller University
TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Catio
TITLE OF INVENTION: Channel Proteins, and Uses Thereof
FILE REFERENCE: 018512-002901US
CURRENT FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: US/09/275,252A
CURRENT FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: US 09/045,529
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 09/043,347
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: WO PCT/US99/06307
PRIOR APPLICATION NUMBER: WO PCT/US99/06307
PRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 858
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                                                                                US-09-275-252A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09275252A Patent No. 6641997 GENERAL INFORMATION:
 Query Match 21.8%; Score 742.5; DB 4; Best Local Similarity 29.1%; Pred. No. 6.7e-62; Matches 194; Conservative 116; Mismatches 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-275-252A-6
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                                                                                                   TYPE: PRT
ORGANISM: Homo
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                                                                                                                                                                                                                                                                                   Sequence 13, Application Patent No. 5710019
                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,34
                                                                                                                                                                                                        APPLICANT: LI, ET AL.
TITLE OF INVENTION: HU
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                 STREET: 6 CAND CITY: ROSELAND STATE: NEW JERSEY 115A
                                                                                                                                                                              ADDRESSEE:
                                                                                                        COUNTRY: UZIP: 07068
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                                                                                                                                                             E: CARELLA, BYRNE, BAIN, GILFILLAN

B: CECCHI, STEWART & OLSTEIN

6 BECKER FARM ROAD
                                                                                                                                                                                                                                       Human Potassium Channel 1 and 2 Proteins
                                                                                                                                                                                                                                                                                                  US/08464340A
  US/08/464,340A
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; TOPOLOGY: LIN:
; MOLECULE TYPE:
US-08-464-340A-13
                                                                                                                                  RESULT 13
US-09-336-643A-4
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                            Sequence 4, Application US/09336643A
Patent No. 6399761
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
              APPLICANT:
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CANT: Rutter, Marc
CANT: Wang, Jian-Wang
OF INVENTION: No. 639976lel Human Potassium Channels
                                                                                                                                                                                                                                                                                                                 366
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 539 AMINO ACIDS
TYPE: AMINO ACID
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ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-415
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 21.2%;
Local Similarity 33.0%;
nes 163; Conservative 9
                                                                                                                                                                                                                                                                                                                        134 ARYHOKKEOMNEELKREAETLREREGEEFDNTCCAEKRKLWDLLEKPNSSVAAKILAIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 DYSLDDNEYFFDRHPGAFTSILNFYRTGRLHMMEEMCALSFSQELDYWGIDEIYLESCCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 MPLAPAD -- KNKRQDELIVLNVSGRRFQT-WRTTLERYPDTLLG-----STEKEFF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFFIAVSVITNVVETVPCGTVPGSKELPCGERYSVA----FFCLDTACVMIFTVEYLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEYKDRKRENAERLMDD----NDSENNQESMPSLSFRQTMWRAFENPHTSTLALVFYYVT
                                                 GKTTSLIESOHHHL 479
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                                                                                                                                               KRRAQKKARLARIRVAKTGSSNAYLHSKRNGLL-----
                                                                                                                                                                                                                          FWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQNQRAD 417
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GKKDKV---QDNHL
                                                                                                                                                                                                FWWATITMTTVGYGDIYPKTLLGKIVGGLCCIAGVLVIALPIPIIVNNFSEFYKEQKRQE
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Pred. No. 1.9e-60;
8; Mismatches 165;
                                                                                                  AKRNGS I VSMNMKDAFARS I EMMD I VVEKNGENM
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245 244 193

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; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
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; TYPE: PRT
; ORGANISM: H.
US-09-336-643A-4
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                                                                                    RESULT 14
US-09-275-252A-4
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Sequence 4, Application US/09275252A Patent No. 6641997 GENERAL INFORMATION: APPLICANT: MacKinnon, Roderick APPLICANT: The Rockefeller Univers.
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Best Local Similarity 31.8%; Pred. No. 4.9e-60;
Matches 192; Conservative 102; Mismatches 221
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 The Rockefeller University
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; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, Mutant Prokaryotic Cation
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/09/275,252A
; CURRENT FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR FILING DATE: 1998-04-02
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
                                                                                                          RESULT 15
US-09-949-016-8164
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Sequence 8164, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 173; Conserv
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TYPE; PRT
ORGANISM: Drosophila melanogaster
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                                                                                                                                                                                 QQSQSP
                                                                                                                                                                                                                                                                                                                                                                                                                       TMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQNQRADKRRAQK 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPASFWYTIV 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNGTKIEEDEVP---DITDPFFLIETLCIIWFTFELTVRFLACPNKLNFCRDVMNVIDII
                                                                                                                                                                                                                     PSTRSP
                                                                                                                                                                                                                                                                                                                                                                KARLARIRVAKTGSSNAYL-----HSKRNGL-----LNEALELTGTPEEEHMGKT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKGLQILGRTLKASMRELGLLIFFLFIGVVLFSSAVYFAEAGSENSFFKSIPDAFWWAVV
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                                                                                                                                                                                                                                                                                         TSLIESOHHHLLHCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEOMFEONCMESSMONY
                                                                                                                                                                                                                                                                                                                            FNHV-----TSCSYLPGALGQHLKKSSLSESSSDIMDLDDGIDATTPGLTDHTGR-
                                                                                                                                                                                                                                                                                                                                                                                                  TMTTVGYGDMTPVGFWGKIVGSLCVIAGVLTIALPVPVIVSNFNYFYHREADREEMQSQN
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                                                                                                                                                                                                                     534
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8164
LENGTH: 552
TYPE: PRT
ORGANISM: Human
US-09-949-016-8164
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Listing first 45 summaries
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AAY13523
AAB86319
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AAW79589

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ADE61252

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Aaw79590 Human Kv
Adf91398 Wild-type
Add48188 Rat Prote
Add18188 Rat Prote
Ads16294 Human Kv4
Abb79585 Human Kv4
Abb79585 Human Kv
Add61252 Rat Prote
Adm10929 Human O64
Adm10928 Human O64
Adm10929 Human O64
Adm10927 Human Ova
Adm11257 Human ova
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Adm43518 Human ova
Adm43521 Human ova
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Ade63538 Rat Prote	Abb57774 Drosophil	Adi38328 Human cat	Aao17058 Human KCN	Aay32015 Human cat	Adj79874 CIKA_huma	Abp58354 Human pot	Adj25645 Voltage-g	Adi30143 Drosophil	Adi30147 Drosophil	Adj69676 Human hea	Adj79875 CIKA_huma	Adm43517 Human ova	Adj11256 Human ova	Adm10926 Human 064	Aay13524 Amino aci	Aab86320 Human Kv4	2 Drosop	Aay34123 Human pot	Aab86318 Human Kv4

## ALIGNMENTS

RESULT 1 ABB79584 Kv4.3; potassium channel; human; Alzheimer's disease; heart disease; nootropic; neuroprotective; cardiant; gene therapy. 01-OCT-2002 ABB79584 standard; protein; Cockett MI, Dilks DW, Ling HC, 23-OCT-1998; 23-OCT-1998; 28-MAY-2002. US6395477-B1. Homo sapiens. Human Kv4.3 potassium channel (long form). ABB79584; (AMHP ) AMERICAN HOME PROD CORP. 2002-556093/59. (first entry) 98US-00178109 98US-00178109 ₿ Sokol PT;

The present sequence is the protein sequence of the long isoform of novel human potassium channel Kv4.3. 2 Isoforms of human Kv4.3 have been identified: the present full-length form (hKv4.3 long); and a second form (see ABB79585), which has a deletion of 19 amino acids in the carboxy domain after the predicted sixth transmembrane domain (hKv4.3 short). Human heart primarily expresses hKv4.3 long, whereas human brain contains both forms. The invention provides Kv4.3 polypeptides, polynucleotides, and methods for producing these polynucleotides. The Kv4.3 polypeptides and polynucleotides are useful in the diagnosis, treatment and screening of human diseases relating to an excess or deficiency of hKv4.3 activity, including Alzheimer's disease and heart disease

New isolated polynucleotide encoding human Kv4.3 potassium channel polypeptide, useful as probe in a diagnostic method for detecting acid encoding human Kv4.3, and for treating Alzheimer's and heart

nucleic

Claim 1; Col 16-20; 19pp; English.

diseases.

N-PSDB;

ABN84400.

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RESULT 2
AAW79590
ID AAW7
XX
AC AAW7
AC AAW7
XX
DT 11-J
XX
DT Huma
XX
POta
KW Pota
KW Pota
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                                                                                                            Potassium
                                                                                                                              Human Kv potassium channel hKv4.3 (longer isoform)
                                                                                                                                                       11-JAN-1999
                                                                                                                                                                                                 AAW79590
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                                           Peptide
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Best Local Similarity
Matches 653; Conserv
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DB; AAV61572.
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                                                        SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPASFWY
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RESULT 3
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                         The invention relates to a nematode worm that expresses a heterologous nucleotide sequence encoding a functional voltage-gated potassium channel of the Kv4 family, or its analog, mutant, variant, homolog, ortholog, part or fragment. The nematode worm is useful in determining whether a compound interacts with the voltage-gated potassium channel of the Kv4 family or whether a compound is an agonist, antagonist, opener and/or blocker of the voltage-gated potassium channel expressed by the nematode worm. The methods are used for identifying and developing compounds that interact with voltage-gated potassium channels of the Kv4 family. The compositions may be used in the development and/or preparation of compositions for pharmaceutical, agrochemical and/or veterinary use.
                                                                                                                                                                                                                                                                                              a functional vol
for determining
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15-MAY-2002; 2002US-0378076P
15-MAY-2002; 2002US-0378131P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antiarrhythmic; cardiovascular; anticonvulsant; cerebroprotective; tranquiliser; sedative; neuroprotective; nootropic; antiparkinsonian; nematode worm; voltage-gated potassium channel; Kv4; agonist; antagonist; blocker; pharmaceutical; agrochemical; veterinary; arrhythmia; tachycardia; congestive heart failure; epilepsy; stroke; traumatic brain injury; anxiety; insomnia; Alzheimer's disease; Parkinson's disease.
These may be used in preparing diseases or conditions such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-2003; 2003WO-IB002453
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VO20
                                                                Rat; pain; neuronal tissue; gene therapy; chronic constriction injury; CCI; spared |
                                                                                                         Rat Protein
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                                                                 ; spinal segmental nerve injury; nerve injury; SNI; Chung.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention discloses a composition comprising two or more isolated rat CC or human polynucleotides or a polynucleotide which represents a fragment, CC derivative or allelic variation of the nucleic acid sequence. Also CC claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence CC which is differentially regulated in an animal subjected to pain and a CC that increases or decreases the expression of the polynucleotide sequence CC subjected to pain, a method for identifying a compound which regulates CC the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially CC expressed in an animal subjected to pain, a method for identifying a compound which regulates the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a continuity in an animal of one or more of the polypoptides given in the CC exivity in an animal of one or more of the polypoptides or their antibodies. The polynucleotide or the compound that composition comprising the one or more pain and a pharmaceutical composition comprising the one or more condulates its activity is useful for preparing a medicament for treating pain decreases its activity is useful for preparing a medicament for treating conjury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (described in Table 3 of the specification, but was obtained in electronic form directly from WIPO at CC fire. WIPO and specification because this patent did not form part of the printed specification contains the printed specification contains the printed specification and spared polypoptical conductors of the printed specification.
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26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
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 YLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGAFVTLRVFRVFRIFKF 300
                                       LALVFYYVTGFFIAVSVITNVVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTVE
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(MACK/) MACKINNON R. (MACK/) MACKINNON A L. (JIAN/) JIANG Y. (RUTA/) RUTA V.

01-MAR-2003; 2003US-00377139 01-MAR-2003; 2003US-00377139 09-SEP-2004

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LRPNCKTSQITTAIISIPTPPALTPEGESRPPPASPGPNTNIPSITSNVVKVSVL
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                                                                 GLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSI
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Best Local
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                                                                                                                                                                                                                                                                                                                                             This invention describes a novel potassium channel protein (I) that is either human Kv4.1 or Kv4.2. Eukaryotic cells that express potassium channels containing (I) are used to identify and test: (i) compounds for treatment of neurodegenerative diseases (autism, epilepsy, ischemia, stroke; Alzheimer's, Parkinson's and Huntington's diseases) or cardiac arrhythmia, or those that improve learning capacity and memory; and (ii) activators of protein kinases. Host cells that express (I) can identify agents that do not interact significantly with channels and control I to (a quickly activated transient current), so lack the side effects of known anti-arrhythmic agents. They also eliminate, or reduce, the need for testing on organ cultures
                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                    MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKRQDELIVLNVSGRRFQTWRTTLER
YLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGAFVTLRVFRVFRIFKF
                                             LALVFYYVTGFFIAVSVITNVVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTVE
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  The present sequence is the protein sequence of the short isoform of novel human potassium channel Kv4.3. 2 Isoforms of human Kv4.3 have been identified: a full-length form (hKv4.3 long) (see ABB79584); and the short form, which has a deletion of 19 amino acids in the carboxy domain after the predicted sixth transmembrane domain (hKv4.3 short). Human heart primarily expresses hKv4.3 long, whereas human brain contains both forms. The invention provides Kv4.3 polypeptides, polynucleotides, and methods for producing these polynucleotides. The Kv4.3 polypeptides and
                                                                                                                                                                                                                                                                                     New isolated polynucleotide encoding human Kv4.3 potassium channel polypeptide, useful as probe in a diagnostic method for detecting acid encoding human Kv4.3, and for treating Alzheimer's and heart
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nootropic; neuroprotective; cardiant;
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DB; ABN84401.
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                                                                                                                                                                                                                    English.
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human diseases relating to an
including Alzheimer's disease
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                                                                                                   HCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMFEQNCMESSMQNYPSTRSPSLSSHP
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                                                                                                                                              AQKKARLARIRVAKTGSSNAYLHSKRNGLLNEALELTGTPEEEHMGKTTSLIESQHHHLL
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                                            GLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDG
                                                    GLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDG
                                                                                                                                                                              TIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQNQRADKRR
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97.1%;
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Pred. No. 1.4e-309;
0; Mismatches 0;
                                                                                     ----NHEFIDEOMFEONCMESSMONYPSTRSPSLSSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the diagnosis, treatment and screening cexcess or deficiency of hKv4.3 activity, and heart disease
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RESULT 8
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AC AAW7
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AC AAW7
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DT 11-J
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DT Huma
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DX Homa
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KW Pota
KW ther
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W OS
EN WO98
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PD 01-C
                                                                               Human
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                                                                                                                                     AAW79589
                                   Homo sapiens
                                                     therapy; diagnosis
                                                             Potassium channel;
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                                                              hKv4.3; human;
                                                                                hKv4.3 (shorter isoform)
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                                                              Alzheimer's disease;
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arrhythmia;

WO9842833-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     channel hKv4.3. The sequence was deduced from an isolated hKv4.3
cpolynucleotide (see AAV61571), and has 99% identity with rat Kv4.3.
chydrophobicity analysis indicates 6 transmembrane domains, typical of all Kv family related proteins. A longer isoform (see AAW79590) has been identified, which has an additional 19 amino acids inserted between amino acids 487 and 488. The invention relates to hKv4.3 polypeptides and polynucleotides, and to methods for producing such polypeptides by recombinant techniques. hKv4.3 polypeptides can be used to identify agonists and antagonists of hKv4.3 polypeptides can be used to identify activity or claimed are methods for utilising such agonists and antagonists for the treatment of subjects in need of enhanced or reduced activity or expression of hKv4.3 polypeptide. These include the treatment of cardiac arrhythmias and Alzheimer's disease. The invention can also be used to to derivity disease associated with inappropriate hKv4.3 expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-1997;
09-DEC-1997;
11-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKRQDELIVLNVSGRRFQTWRTTLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the amino acid sequence for an isoform of human Kv
                                                                                                                                                                                                                                                             LALVFYYVTGFFIAVSVITNVVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTVE
AQKKARLARIRVAKTGSSNAYLHSKRNGLLNEALELTGTPEEEHMGKTTSLIESQHHHLL
                                                                              TIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQNQRADKRR
                                                                                                                                  SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPASFWY
                                                                                                                                                                             YLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGAFVTLRVFRVFRIFKF
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                                                                                                                                                                                                                                          LALVFYYVTGFFIAVSVITNVVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTVE
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                                                                                                                 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPASFWY
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97EP-00402971.
97EP-00403007.
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                                  This is the amino acid sequence for an isoform of human Kv potassium channel hKv4.3. The sequence was deduced from an isolated hKv4.3. C polynucleotide (see AAV61573), and has 98% identity with rat Kv4.3. C polynucleotide (see AAV61573), and has 98% identity with rat Kv4.3. C polynucleotide proteins hKv4.3 isoforms (see AAW79599 and AAW79590) C are also claimed. The invention relates to hKv4.3 polypeptides and C polynucleotides, and to methods for producing such polypeptides by recombinant techniques. hKv4.3 polypeptides can be used to identify C agonists and antagonists of hKv4.3 polypeptides can be used to identify C agonists are methods for utilising such agonists and antagonists for the C treatment of subjects in need of enhanced or reduced activity or expression of hKv4.3 polypeptide. These include the treatment of cardiac arrhythmias and Alzheimer's disease. The invention can also be used to to detect disease associated with inappropriate hKv4.3 expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-1997;
09-DEC-1997;
11-DEC-1997;
                                                                                                                                                                                                                                                                                   New potassium channel polypeptides, hKv4.3 poly:nucleotide(s) useful in the treatment arrhythmias and Alzheimer's disease.
                                                                                                                                                                                                                                                          Claim 19; Page 28; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-542277/46.
N-PSDB; AAV61573.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDG
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97EP-00402971.
97EP-00403007.
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Query Match Best Local

Similarity

96 95 .7%;

Score Pred.

3265.5; DB 2; No. 3.4e-306;

Length 636;

Sequence

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RESULT 10
ADE61252
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01-NOV-2001;
26-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                 Rat; pain;
chronic cor
                                                                                                                                                            14-AUG-2002;
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                                                                                                                                                                                                                                                                                                              Rattus norvegicus.
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                                                                                                                                                                                                                                                                                                                                                          neuronal tissue; gene therapy; spinal segmental nerve injury; nstriction injury; CCI; spared nerve injury; SNI; Chung.
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      HOSPITAL
                                                     2001US-0312147P.
2001US-0346382P.
2001US-0333347P.
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The invention discloses a composition comprising two or more isolated rat CC or human polynucleotides or a polynucleotide which represents a fragment, CC derivative or allelic variation of the nucleic acid sequence. Also Cc claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence Which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent CC that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially composition and that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating compound that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more compound that segmental nerve injury (CMung), chronic constriction conjury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification, which is differentially expressed during pain. Note: specification, which is differentially expressed during pain. Note: specification, but was obtained in electronic form directly from WIPO at ftp. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New composition comprising preparing a medicament for
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Query Match Best Local : Sequence 611 AA; 89.0%; Score 3035.5; DB 7. Pred. No. 5.8e-284; 2; Mismatches 2; 7; Length

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                                                                                                                                                             LALVFYYVTGFFIAVSVITNVVETVPGGTVPGSKELPCGERYSVAFFCLDTACVMIFTVE
TIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQNQRADKRR
                                                            SRHSQGIRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPASFWY
                                                                                                               YLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGAFVTLRVFRVFRIFKF
                                                                                                                                                LALVFYYVTGFFIAVSVITNVVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTVE
                                                                                                                                                                                                                 YGILPEIIGDCCYEEYKDRKRENAERLMDDNDSENNQESMPSLSFRQTMWRAFENPHTST
                                                                                                                                                                                                                                                                                                 MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKRQDELIVLNVSGRRFQTWRTTLER
                                                 SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPASFWY
                                                                                                  YLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGAFVTLRVFRVFRIFKF
                                                                                                                                                                                                 YGIHPEIIGDCCYEEYKORKRENAERLMDDNESENNQESMPSLSFRQTMWRAFENPHTST
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RESULT 11
ADM10929
ID ADM10
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AC ADM10
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DT 20-MA
XX
DT 20-MA
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Ovari
KW cytos
XX
Cytos
XX
O6-NC
XX
O6-NC
PD 06-NC
XX
O7-SE
PR 11-NC
PR 01-M2
PR 07-SE
PR 11-NC
PR 07-SE
PR 11-NC
PR 07-AL
PR 11-NC
PR 07-AL
PR 07-AL
PR 11-NC
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        This invention describes a novel ovarian tumour protein which can be us to detecting the presence of an ovarian cancer in a patient by stimulating and/or expanding T cells specific for the tumour protein. T products of the invention can also be used in a method to inhibit the development of a cancer in a patient comprising (a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one ovarian tumour protein, such that T cell proliferate and (b) administering to patient the proliferated T cells. The cytostatic polynucleotides or polypeptides described in the invention are useful for treating or inhibiting the development of cancer, particularly ovarian cancer and inhibiting the development of cancer, particularly ovarian cancer and
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01-MAY-2000;
15-AUG-2000;
07-SEP-2000;
14-NOV-2000;
03-APR-2001;
02-OCT-2001;
02-AUG-2002;
stimulating and/or expanding gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ovarian; tumour protein; cancer; T cell; CD4+ cell; cytostatic; gene therapy; human; ds.
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2000US-00561778.

2000US-00640173.

2000US-00656668.

2000US-00713550.

2001US-00825294.

2001US-00970966.

2002US-00212677.
                                                                                                                                                                                                         SEQ ID NO 260;
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RESULT 12
ADM10928
ID ADM10
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AC ADM10
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DT 20-MA
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DE Human
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Cytos
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Best Local Similarity 73.6%;
Matches 486; Conservative 6
                                                                                       ovarian; tumour protein; cancer;
cytostatic; gene therapy; human;
          05-FEB-2003; 2003US-00361811
                               06-NOV-2003.
                                                                                                                      Human 0647SgenomicContig3 homologue protein
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Pred. No. 5.5e
59; Mismatches
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Matches 486
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01-MAY-2000; 2000US-00561778.
15-AUG-2000; 2000US-00640173.
07-SEP-2000; 2000US-00656668.
14-NOV-2000; 2000US-00713550.
03-APR-2001; 2001US-00825294.
02-OCT-2001; 2001US-00970966.
02-AUG-2002; 2002US-00212677.
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DB; ADM10922.
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                      KRRAQKKARLARIRVAKTGSSNAYLHSKRNGLLNEALELTGTPEEEHMGKTTSLIESQHH
                                                                                                                               FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPAS
                                                                                                                                                                                       TVEYLLRLFÄAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGAFVTLRVFRVFRI
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KRRAQKKARLARIRAAKSGSANAYMQSKRNGLLSNQLQ-SSEDEQAFVSKSGSSFETQHH
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73.6%;
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RESULT 13
ADM10930
ID ADM10
XX ADM10
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AC
                                 CC This invention describes a novel ovarian tumour protein which can be used to detecting the presence of an ovarian cancer in a patient by CC stimulating and/or expanding T cells specific for the tumour protein. The products of the invention can also be used in a method to inhibit the CC development of a cancer in a patient comprising (a) incubating CD4+ CC and/or CD8+ T cells isolated from a patient with at least one ovarian CC tumour protein, such that T cell proliferate and (b) administering to the CC patient the proliferated T cells. The cytostatic polynucleotides or polypeptides described in the invention are useful for treating or inhibiting the development of cancer, particularly ovarian cancer and for stimulating and/or expanding T cells specific for a tumour protein or for CC gene therapy.
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01-MAY-2000; 2000US-00561778.
15-AUG-2000; 2000US-00640173.
07-SEP-2000; 2000US-0065668.
14-NOV-2000; 2000US-00713550.
03-APR-2001; 2001US-00825294.
02-OCT-2001; 2001US-00970966.
02-AUG-2002; 2002US-00212677.
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Score Pred.

2498.5; DB 7 No. 5.5e-232;

Length

Query Match

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PR 15-A1
PR 11-N0
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01-MAY-2000;
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07-SEP-2000;
14-NOV-2000;
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                                                                        05-FEB-2003; 2003US-00361811
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Matches 486
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02-AUG-2002;
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15-AUG-2000; 2000US-00640173.

07-SEP-2000; 2000US-00656668.

14-NOV-2000; 2000US-00713550.

03-APR-2001; 2001US-00825294.

02-OCT-2001; 2001US-00970966.

02-AUG-2002; 2002US-00212677.

05-FEB-2003; 2003US-00361811.
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1257
                                                                                                             This invention relates to novel isolated polynucleotides and methods for the therapy and diagnosis of cancer, particularly ovarian cancer. Specifically, it refers to these polynucleotides and the encoded polypeptides thereof, as well as immunogenic peptides, antibodies, antigen presenting cells (APCs) and immune system cells (e.g. T cells) that are targeted to those cells expressing the proteins of interest. The present invention describes methods that are useful for stimulating and/or expanding T cells specific for a tumourigenic protein (i.e. T cell therapy). Furthermore, compositions can be used for the diagnosis, treatment and/or prevention of ovarian cancer by stimulating an immune response in a patient. Accordingly, these compositions exhibit cytostatic activity. This polypeptide is a human ovarian tumour antigen protein sequence given in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human;
APC; in
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                                                                                                                                                                                                                                                                                                                                                   Novel isolated ovarian polypeptide, useful as in a patient.
                                                                                     Sequence 630
                                                                                                                                                                                                                                                                                                                       Example 12; SEQ ID NO 258; 222pp; English.
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N-PSDB; ADJ11251.
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                           Score 2498.5; DB 8;
Pred. No. 5.5e-232;
9; Mismatches 70;
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                                                                                                                                                                                                                                                                                                          FYGILPEIIGDCCYBEYKDRKRENAERIMDDNDSENNQES-MPSLSFRQTMWRAFENPHT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYPDTLLGSSERDFFYHPETQQYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDEELA
                                                                                                                                                                  KRRAQKKARLARIRVAKTGSSNAYLHSKRNGLLNEALELTGTPEEEHMGKTTSLIESQHH
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EECVKLNCEQPYVTTAIISIPTPPVTTPEGDDRPESPEYSGG-----NIVRVSAL
                                                  SQQGVTSTCCSRRHKKTFRIPNANVSGSHQGSIQELSTIQIRCVERTPLSNSRSSLNAKM
                                                                          SHPGLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKA 597
                                                                                                    KRRAQKKARLARIRAAKSGSANAYMQSKRNGLLSNQLQ-SSEDEQAFVSKSGSSFETQHH
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Search completed: April Job time: 501.211 secs 6 2005, 06:53:18

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

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Result
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Listing first 45 summaries
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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US-10-361-811-258
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Sequence 2, Appli
Sequence 4, Appli
Sequence 25, App
Sequence 259, App
Sequence 260, App
Sequence 261, App
Sequence 259, App
Sequence 259, App
Sequence 250, App
Sequence 261, App
Sequence 258, App
Sequence 259, App
Sequence 259, App
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ALIGNMENTS

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e 75, e 33, e 32, e 2015	960,	Sequence 4, Appli Sequence 27, Appli Sequence 8, Appli	2, 2, 175	Sequence 5, Appli Sequence 4, Appli Sequence 13, Appl		e 148	13, 51	

## Sequence 2, Application US/10062879 | Sequence 2, Application No. US20020127649A1 | GENERAL INFORMATION: | APPLICANT: Cockett, Mark I. | APPLICANT: Dilks, Daniel W. | APPLICANT: Chang Ling, Huai-Ping | APPLICANT: Sokol, Patricia T. | TITLE OF INVENTION: Human Potassium Channel Polynucleotides and | TITLE OF INVENTION: Polypeptides and Uses Therefor | FILE REFERENCE: ahp-98089 | CURRENT APPLICATION NUMBER: US/10/062,879 | CURRENT FILING DATE: 2002-01-31 | PRIOR APPLICATION NUMBER: US/09/178,109 | PRIOR FILING DATE: 1998-10-23 | NUMBER OF SEQ ID NOS: 4 | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NO 2 | LENGTH: 655 | TYPE: PRT | ORGANISM: human | US-10-062-879-2 밁 S В S US-10-062-879-2 RESULT 1 Query Match Best Local Similarity Matches 655; Conserv 61 61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF 120 1 MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKRQDELIVLNVSGRRFQTWRTTLER MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKRQDELIVLNVSGRRFQTWRTTLER 100.0%; Score 3412; DB 13; ilarity 100.0%; Pred. No. 1.3e-283; Conservative 0; Mismatches 0; 1 Indels Length 655; 0; Gaps

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Sequence 6, Application US/10377139;
Publication No. US20040175761A1
GENERAL INFORMATION:
APPLICANT: MacKinnon, Roderick
APPLICANT: Lee MacKinnon, Alice
APPLICANT: Ruta, Youxing
APPLICANT: Ruta, Vanessa
TITLE OF INVENTION: Voltage Sensor Domains of
FITLE OF INVENTION: Uses Thereof
FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
CURRENT APPLICATION NUMBER: US/10/377,139
CURRENT FILING DATE: 2003-03-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SOFTWARE: PatentIn version 3.1
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                                                             YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF
                                                                                                    LRPNCKTSQITTAIISIPTPPALTPEGESRPPPASPGPNTNIPSITSNVVKVSVL 655
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YGILPEIIGDCCYEEYKORKRENAERLMDDNDSENNQESMPSLSFRQTMWRAFENPHTST
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                                              YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF
                                                                                                                                                                  Conservative
                                                                                                                                                                             99.5%;
                                                                                                                                                           Score 3395; DB 16;
Pred. No. 3.7e-282;
0; Mismatches 2;
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APPLICANT: Dilks, Daniel W.

APPLICANT: Chang Ling, Huai-Ping

APPLICANT: Sokol, Patricia T.

TITLE OF INVENTION: Human Potassium Channel Polynucleotides and

TITLE OF INVENTION: Polypeptides and Uses Therefor

FILE REFERENCE: ahp-98089

CURRENT APPLICATION NUMBER: US/10/062,879

CURRENT FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: US/09/178,109

PRIOR APPLICATION NUMBER: US/09/178,109

PRIOR APPLICATION NUMBER: US/09/178,109

SEQ ID NOS: 4

SOPTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 636
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US-10-062-879-4
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Best Local Similarity
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 YGILPEIIGDCCYEEYKDRKRENAERLMDDNDSENNQESMPSLSFRQTMWRAFENPHTST
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                                                                                                                                                                  Conservative
                                                                                                                                                                             96.7%;
97.1%;
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Pred. No. 4.6e-274;
0; Mismatches 0; 1
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655 655

> 600 600 540

540 480

19;

Gaps

180

120

237

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APPLICANT: Chenault, Ruth A.

APPLICANT: Chenault, Ruth A.

APPLICANT: Chenault, Ruth A.

APPLICANT: Chenault, Ruth A.

APPLICANT: Fanger, Gary R.

APPLICANT: Harlocker, Susan L.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.484C7

CURRENT APPLICATION NUMBER: US/10/212,677

CURRENT FILING DATE: 2002-08-02

NUMBER OF SEQ ID NOS: 288

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 258

LENGTH: 630

TYPE: PRT

ORGANISM: Homo sapiens

US-10-212-677-258
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US-10-212-677-258
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; Publication No. U
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Matches 486
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GLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDG
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                                                                                                         MAAGVAAWLPFARAAAIGWMPVASGPMPAPPRQERKRTQDALIVLNVSGTRFQTWQDTLE
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                                                                                                                                                               Conservative
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                                                                                                                                                                        73.2%;
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                                                                                                                                                             Score 2498.5; DB 14; Length Pred. No. 3.1e-205; Mismatches 70; Indels
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; Sequence 259, Application US/10212677
; Publication No. US20030129192A1
; GENERAL INFORMATION:
; APPLICANT: Chenault, Ruth A.
APPLICANT: Xu, Jiangchun
; APPLICANT: Fanger, Gary R.
APPLICANT: Harlocker, Susan L.
APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C7
; CURRENT APPLICATION NUMBER: US/10/212,677
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
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630 655 580

597 520 537 479 477 420 417 360 357 300

Indels Length

35; 630;

Gaps

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Sequence 260, Application US/10212677

Fublication No. US20030129192A1

GENERAL INFORMATION:
APPLICANT: Chenault, Ruth A.
APPLICANT: Ku, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.4846C7
CURRENT APPLICATION NUMBER: US/10/212,677
CURRENT FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 288
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 260
LENGTH: 630
TYPE: PRT
ORGANISM: Homo sapiens
US-10-212-677-260
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US-10-212-677-260
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APPLICANT: Chenault, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Gary R.
APPLICANT: Harlocker, Susan L.
APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C7
CURRENT APPLICATION NUMBER: US/10/212,677
CURRENT APPLICATION E 2002-08-02
NUMBER OF SEQ ID NOS: 288
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 261
LENGTH: 630
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US-10-212-677-261
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; ORGANISM: Homo sapiens
US-10-212-677-261
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Best Local Similarity
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STLALVFYYVTGFFIAVSVITNVVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF
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                                                   FFGLIPEIIGDCCYEEYKDRRRENAERLQDDADTDTAGESALPTMTARQRVWRAFENPHT
                                                                                                                                                                                                                                                     73.2%; Score 2498.5; 73.6%; Pred. No. 3.16 ative 69; Mismatches
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APPLICANT: Fanger, Gary R.

APPLICANT: Fling, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CAN FILE REFERENCE: 210121.484CB

CURRENT APPLICATION NUMBER: US/10/361,811

CURRENT FILING DATE: 2003-02-05

NUMBER OF SEQ ID NOS: 293

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 258
                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo s
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Best Local Similarity
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                                           FYGILPEIIGDCCYEEYKDRKRENAERLMDDNDSENNQES-MPSLSFRQTMWRAFENPHT
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Pred. No. 3.1e-205;
59; Mismatches 70; II
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US-10-361-811-259
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CURRENT FILING DATE: 2003-02-05
NUMBER OF SEQ ID NOS: 293
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 259, Application US/10361811
Publication No. US20030206918A1
GENERAL INFORMATION:
APPLICANT: Fanger, Gary R.
APPLICANT: Fiing, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C8
                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                  RYPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELA 119
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APPLICANT: FAIRGER, GARY R.

APPLICANT: FLING, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.484C8

CURRENT APPLICATION NUMBER: US/10/361,811

CURRENT FILING DATE: 2003-02-05

NUMBER OF SEQ ID NOS: 293

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 260

LENGTH: 630

TYPE: PRT

ORGANISM: Homo sapiens

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Best Local Similarity 73.6%;
Matches 486; Conservative 6
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o. US20030206918A1
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Publication No. US20030206918A1

GENERAL INFORMATION:
APPLICANT: Fanger, Gary R.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.484C8
CURRENT APPLICATION NUMBER: US/10/361,811
CURRENT FILING DATE: 2003-02-05
NUMBER OF SEQ ID NOS: 293
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 261
LENGTH: 630
TYPE: PRT
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US-10-361-811-261
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73.6%; Pred. No. 3.1e-205;
Live 69; Mismatches 70;
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CAPTILE REFERENCE: 210121.484C9; FILE REFERENCE: 210121.484C9; CURRENT APPLICATION NUMBER: US/10/369,186; CURRENT FILING DATE: 2003-02-14; NUMBER OF SEQ ID NOS: 293; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 258; LENGTH: 630; TYPE: PRT

ORGANISM: Homo sapiens
US-10-369-186-258
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US-10-369-186-258
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Publication No. US20030232056
GENERAL INFORMATION:
APPLICANT: Fanger, Gary R.
APPLICANT: Fling, Steven P.
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Similarity 73.6%;
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 HLLHCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMFEQNCMESSMQNYPSTRSPSLS
                                                     KRRAQKKARLARIRAAKSGSANAYMQSKRNGLLSNQLQ-SSEDEQAFVSKSGSSFETQHH
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o. US20030232056A1
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US-10-369-186-259
; Sequence 259, Application US/10:
; Publication No. US20030232056A1
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APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C9
CURRENT APPLICATION NUMBER: US/10/369,186
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 293
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 259
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TYPE: PRT
ORGANISM: Homo :
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RESULT 14
US-10-369-186-260
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-186-260
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APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C9
CURRENT APPLICATION NUMBER: US/10/369,186
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 293
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 260
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Best Local Similarity
Matches 486; Conserv
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APPLICANT: Fling, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE

FILE REFERENCE: 210121.484C9

CURRENT APPLICATION NUMBER: US/10/369,186

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 293

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 261

LENGTH: 630
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US-10-369-186-261
; Sequence 261, Ap
; Publication No.
; Publication INFORMAT
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; ORGANISM: Homo sapiens
US-10-369-186-261
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                                                                  DDG1RPNCKTSQITTAIISIPTPPALTPEGESRP--PPASPGPNTNIPSITSNVVKVSVL
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                                                                                                                                 SHPGLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKA
                                                                                                                                                                                              HLLHCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMFEQNCMESSMQNYPSTRSPSLS
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                                                                                                            SQQGVTSTCCSRRHKKTFRIPNANVSGSHQGSIQELSTIQIRCVERTPLSNSRSSLNAKM
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3: pir3:*
4: pir4:*
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Maximum Match 100%
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20.2	20.3	20.3	20.3	20.4	20.4	20.4	20.5	20.5	20.5	20.5	20.6	20.6	20.7	20.7	20.7
558	654	653	581	660	499	625	624	499	489	679	498	495	597	476	495
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T23991	S11049	A39922	S17150	S24125	A48672	S13919	S22703	JH0313	JC4787	A42073	A41359	I57680	S51212	S21144	B39113
hypothetical prote	potassium channel	potassium channel	potassium channel	potassium channel	delayed rectifier	potassium channel	voltage-gated pota	potassium channel	shaw protein - Cal	potassium channel	potassium channel	potassium channel	BAKS protein - bov	potassium channel	potassium channel

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N;Alternate names: rat sha/1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
C;Date: 3100271; A39113
C;Accession: JU0271; A39113
R;Baldwin, T.J; Tsaur, M.L.; Lopez, G.A.; Jan, Y.N.; Jan, L:Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Description: this protein forms a 4-amino-pyridine-sensitive potassium channel (valida C; Superfamily: potassium channel protein drkl C; Keywords: channel-forming protein; ion channel; phosphoprotein; potassium channel C; Keywords: channel-forming protein; ion channel; phosphoprotein; potassium channel p; 54,280,489,606/Binding site: phosphate (Thr) (covalent) (by casein kinases) #sta p; 54,280,489,606/Binding site: phosphate (Thr) (covalent) (by grotein kinase C) #status p; 101,166,291,316/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status p; 113,263,459,460,472,502,552/Binding site: phosphate (Ser) (covalent) (by casein kinase F; 113,263,459,460,472,502,552/Binding site: phosphate (Ser) (covalent) (by casein kinase F; 1592/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: hippocampus
R;Roberds, S.L.; Tamkun, M.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
A;Title: Cloning and tissue-specific expression of five voltage-gated potassium channel A;Reference number: A39113; MUID:91156694; PMID:1705709
A;Accession: A39113
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A;Residues: 1-476,'T','P',603-604,'ASL',608,'GENHE',614 <ROB>
A;Cross-references: GB:M59980; NID:g203467; PIDN:AAA40929.1; PID:g203468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-630 <BAL>
A;Cross-references: UNIPROT:Q63881; GB:S64320; NID:g236196; PIDN:AAB19939.1; PID:g236197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuron 7, 471-483, 1991
A;Title: Characterization of a mammalian cDNA for an inactivating voltage-sensitive A;Reference number: JU0271; MUID:92000693; PMID:1840649
A;Accession: JU0271
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FYGILPEIIGDCCYEEYKDRKRENAERLMDDNDSENNQES-MPSLSFRQTMWRAFENPHT 178
                                                                                                   RYPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELA 119
                                                                                                                                                                                           MAAGVAAWLPFARAAAIGWMPVASGPMPAPPRQERKRTQDALIVLNVSGTRFQTWQDTLE
                                                                  RYPDTLLGSSERDFFYHPETQQYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDEELA
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                                                                                                                                                                                                                                                                                                                                                   73.3%;
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Pred. No. 1.1e-182;
9; Mismatches 70;
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RESULT 2
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A39372
C;Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
R;Pak, M.D.; Baker, K.; Covarrubias, M.; Butler, A.; Ratcliffe, A.; Salkoff, L.
Proc. Natl. Acad. Sci. U.S.A. 88, 4386-4390, 1991
A;Title: mShal, a subfamily of A-type K(+) channel cloned from mammalian brain.
A;Reference number: A39372; MUID:91239573; PMID:2034678
A;Accession: A39372
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-651 <PAK>
A;Cross-references: UNIPROT:Q03719; GB:M64226; NID:g199812; PIDN:AAA39745.1; PID:g199813
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                                                                                          HTSTLALVFYYVTGFFIAVSVITNVVETVPCGTVP--GSKELPCGERYSVAFFCLDTACV
                                                                                                                                            YGLVPELVGDCCLEEYRDRKKENAERLAEDEEAEQAGEG-PALPAGSSLRQRLWRAFENP
                                                                                                                                                                                YGILPEIIGDCCYEEYKDRKRENAERLMDDNDSENNQESMPSL----SFRQTMWRAFENP
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                                                                                                                                                                                                                                                                                 A35312
potassium channel protein Shal2 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 14-Sep-1990 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C;Accession: A35312; S12747
R;Wei, A.; Covarrubias, M.; Butler, A.; Baker, K.; Pak, M.; Salkoff, L.
Science 248, 599-603, 1990
A;Title: K+ current diversity is produced by an extended gene family conserved i A;Accession: A35312
A;Accession: A35312
A;Molecule type: mRNA
A;Residues: 1-490 <WEI>
A;Cross-references: UNIPROT:P17971; GB:M32660; NID:g158456; PID:g158457
A;Cross-references: UNIPROT:P17971; GB:M32660; NID:g158456; PID:g158457
A;Cross-references: UNIPROT:P17971; GB:M32660; NID:g158456; PID:g158457
A;Accession: S12746
A;Accession: S12746
A;Accession: S12746; MUID:90245668; PMID:2336395
A;Accession: S12746
A;Cross-references: EMBI:M32660; NID:g158456; PID:g158457
C;Genetics:
A;Gene: shal2
A;Cross-references: ENBI:M32660; NID:g158456; PID:g158457
C;Keywords: alternative splicing; ion channel; potassium channel; transmembrane
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                     YGILPEIIGDCCYEEYKDRKRENAERLMDDNDSENNQESMPSL-SFRQTMWRAFENPHTS
                                                                       YPDTLLGSNEREFFYDEDCKEYFFDRDPDIFRHILNYYRTGKLHYPKHECLTSYDEELAF
                                                                                                                                              ASVAAWLPFARAAAIGWVPIATHPLPPPPMPKDRRKTDDEKLLINVSGRRFETWRNTLEK
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   FGIMPDVIGDCCYEDYRDRKRENAERLMDDKLSENGDQNLQQLTNMRQKMWRAFENPHTS
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RESULT 5
JH0595
JH0595
C; Species: Rattus norvegicus (Norway rat)
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change
C; Accession: JH0595
R; Hwang, P.M.; Glatt, C.E.; Bredt, D.S.; Yellen, G.; Snyder, S.H
Neuron 8, 473-481, 1992
A; Title: A novel K+ channel with unique localizations in mammali
A; Reference number: JH0595; MUID:92198655; PMID:1550672
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A;Title: Families of potassium channel genes in ma A;Reference number: I57681
A;Accession: I57681
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A; Residues: 1-236 < RES>
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C;Species: Rattus norvegicus (Norway rat)
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 novel K+ channel with unique localizations in mammalian number: JH0595; MUID:92198655; PMID:1550672
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Pred. No. 1.1e-76;
2; Mismatches 14;
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A;Accession: JH0595
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-802 <HWA>
A;Cross-referencės: GB:M77482; NID:g203395; PIDN:AAA40905.1; PID:g203396
A;Cross-referencės: GC:M77482; NID:g203395; PIDN:AAA40905.1; PID:g203396
A;Experimental source: circumvallate papillae
C;Superfamily: potassium channel protein drkl
C;Superfamily: potassium channel protein drkl
C;Keywords: glycoprotein; phosphoprotein; transmembrane protein
F;191-212/Domain: transmembrane #status predicted <TM1>
F;233-254/Domain: transmembrane #status predicted <TM2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 LRILKLARHSTGLQSLGFTLRRSYNELGLLILFLAMGIMIFSSLVFFAEKDEDATKFTSI
                                                                                                                                     --MLYNEITKTQTHSHPNPDCQEQPERPSAYEEEIEMEEVVCPQEQLAVAQTEVIVDMKS
                                                                                                                                                                      SYLVDDPLLSVRTSTIKNHEFIDE------QMFEQNCMESSM---QNYPSTRSPS
                                                                                                                                                                                                                                         SKRNGLLNEAL------ELTGTPEEEHMGKTTSLIESQHHHLLHCLEKTTGL
                                                                                                                                                                                                                                                                                                                                              LLRFLSSPNKWKFFKGPLNVIDLLAILPYYVTIFLTESNKSVLQFQNVRRVVQIFRIMRI
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SRDKG--PAAREAALDYAPIDITVNLDAGASHGPLQPDSASDSPKSSLKG--SNPLK
                            KADDGLRPNCKTSQITTAIISIPTP-PALTPEGESRPPPASPGPNTNIPSITSNVVK
                                                                                                 LSSHPGLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNL 595
                                                                                                                                                                                                                                                                                                              RADK----RRAQKKAR-----NAYLH
                                                                                                                                                                                                                                                                                                                                                                                                                                      FRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNN-----EDVSGAFVTLRVFRV
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                                                                                                                                                                                                        PSRWKWARKALSETSSNKSYENKYQEVSQKDSHEQLNNTSS--SSPQHLSAQKLE----
                                                                                                                                                                                                                                                                            RQEKAI KRREALERAKRNGSI VSMNLKDAFARSMELI DVAVEKAGESANI KDSVDDNHLS
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%; Pred. No. 2.9e-50;
123; Mismatches 263
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RESULT 6 \$31761 potassium channel protein C;Species: Homo sapiens (m

DRK1

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potassium c
C;Species:
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CHRTD1
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C;Accession: S1761
C;Accession: S1761
A;Accession: Cloning, expression and chromosomal localization A;Accession: S31761
A;Accession: S31761
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,Residues: 1-858 <ALB>
,Cross-references: UNIPROT:Q14721; EMBL:X68302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene: GDB:KCNB1; KV2.1; DRK1; Cross-references: GDB:128081; OMIM:600397; Map position: 20q13.2-20q13.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: potassium channel protein drkl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
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  channel: Rattus
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                                                                                                                   ILNTKESAAQSKPKEEL--
                                                                                                                                         SLTTSRSSLNLKADDGLRPNCKTSQITTAIISIPTPPALTPEGESRPPPASPGPNTNIPS
                                                                                                                                                                                      MONYPSTRSPSLSSHPGLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQP
                                                                                                                                                                                                                                                            EKAIKRREA-LER----
                                                                                                                                                                                                                                                                                                        SFWWATITMTTVGYGDIYPKTLLGKIVGGLCCIAGVLVIALPIPIIVNNFSEFYKEQKRQ
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                                                                                                                                                                                                             MGKKDKV---QDNHLSPNKWKWTKRT-----LS-ETSSSKS-----FETK
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 protein dr)
                                                                                             650
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             drk1
 (Norway
                                                                                                                                                                                                                                                            -----AKRNGSIVSMNMKDAFARSIEMMDIVVEKNGEN
   rat)
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'MPAG',1-571 <DRE>
A;Residues: 'MPAG',1-571 <DRE
A;Residues: 'MPAG',1-571 <DRE>
A;Residues: 'MPAG',1-571 <DRE
A;Residues: 'MPAG',1-571 <DRE
A;Residues: 'MPAG',1-571 <DRE
A;Residues:
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C;Accession: S05448; A44838
R;Frech, G.C.; VanDongen, A.M.J.; Schuster, G.; Brown, A.M.; Joho, R.H.
Nature 340, 642-645, 1989
A;Title: A novel potassium channel with delayed rectifier properties isolated from A;Reference number: S05448; MUID:89365157; PMID:2770868
A;Recession: S05448
A;Accession: A44838; MUID:92156897; PMID:1740690
A;Accession: A44838; MUID:92156897; PMID:1740690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -FNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAFYGILPEIIGDCCY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGFFIAVSVITNVVETVPCGTVPGSKELPCGERYSVA----FFCLDTACVMIFTVEYLL
                                                                                        EKAIKRREALERAKRNGSIVSMNMKDAFARSIEMMDIVVEKNGESIAKKDKVQDNHLSPN
                                                                                                                                                                        DK----RRAQKKAR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPA
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-TPEEEHMGKTTSLIESQHHHLLHCLEKTTGLSYLVDDPLLS
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Pred. No. 2.8e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                            -LARIRVAKTGSSNA-----YLHSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266; Indels
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41

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JH0166

potassium voltage-gated channel - rat
N;Alternate names: potassium channel KV1; potassium channel RK4; shaker-related pot
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: JH0166; D39113; I55392
R;Swanson, R.; Marshall, J.; Smith, J.S.; Williams, J.B.; Boyle, M.B.; Folander, K.
Neuron 4, 929-939, 1990
A;Title: Cloning and expression of cDNA and genomic clones encoding three delayed:

**The formact number: JH0166; MUID:90297965; PMID:2361015
                                                                                                                                                                     A;Gene: KV1.5

C;Superfamily: potassium channel protein drk1
C;Keywords: glycoprotein; phosphoprotein; potassium channel; transmembra F;242-260/Domain: transmembrane #status predicted <TM1>
F;316-336/Domain: transmembrane #status predicted <TM2>
F;347-368/Domain: transmembrane #status predicted <TM3>
F;387-408/Domain: transmembrane #status predicted <TM4>
F;423-444/Domain: transmembrane #status predicted <TM5>
F;423-444/Domain: transmembrane #status predicted <TM6>
F;403-444/Domain: transmembrane #status predicted <TM6>
F;404-505/Domain: transmembrane #status predicted <TM6>
F;10,44,116,181,290/Binding site: carbohydrate (Asn) (covalent) #status F;81,535,546,569/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-552, 'S', 554-602 < ROB>
R; Mori, Y.; Matsubara, H.; Folco, E.; Siegel, A.; Koren, G.
J. Biol. Chem. 268, 26482-26493, 1993
A; Title: The transcription of a mammalian voltage-gated potassium channel A; Reference number: 155392; MUID:94075338; PMID:8253777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Roberds, S.L.; Tamkun, M.M.

Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
A;Title: Cloning and tissue-specific expression of five A;Reference number: A39113; MUID:91156694; PMID:1705709
A;Accession: D39113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
JH0166
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-15 <RES>
A;Cross-references: GB:L23434; NID:g443766; PIDN:AAA42337.1;
A;Experimental source: Sprague-Dawley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-602 <SWA>
A;Cross-references: UNIPROT:P19024; GB:M27158; NID:g205100;
A;Experimental source: Trial
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                                                                                                  21.6%;
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                                                                       Score 736; DB 2;
Pred. No. 4.1e-48;
90; Mismatches 162
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potassium channel protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26
C;Accession: I56529
R;Pak, M.D.; Covarrubias, M.; Ratcliffe,
J. Neurosci. 11, 869-880, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
I56529
                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q03717; GB:M64228
C;Genetics:
A;Gene: Shab
C;Superfamily: potassium channel protein drk1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: A mouse brain homolog of the Drosophila Shab K A;Reference number: I56529; MUID:91162315; PMID:2002364 A;Accession: I56529
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Best Local Similarity 27.3%; Pred. No. 8e-48;
Matches 205; Conservative 131; Mismatches 2
195
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                                                                                                                                              75
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                                                                                                          EEYKDRKRENAERLMDDNDSENNQE-----SMPSLSFRQTMWRAFENPHTSTLALVFYYV 188
                                                                                                                                                                                                                                             MPLAPAD--KNKRQDELIVLNVSGRRFQT-WRTTLERYPDTLLG----STEKEFF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLAILRVIRLVRVFRIFKLSRHSKGLQILGKTLQASMRELGLLIFFLFIGVILFSSAVYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIFTVEYLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MDDNDSENNQESMPSLSFRQTMWRAFENPHTSTLALVFYYVTGFFIAVSVITNVVETVP-
SIMFIVLSTIALSLNTLP--
                                 TGFFIAVSVITNVVETVPCGTVPGSKELPCGERYSVA-----FFCLDTACVMIFTVEYLL 243
                                                                                                                                              DYSLEDNEYFFDRHPGAFTSILNFYRTGRIHMMEEMCALSFSQELDYWGIDEIYLESCCQ 134
                                                                                                                                                                                                                     LPPEPMEIVRSKACSRRVRLNVGGLAHEVLWR-TLDRLPRTRLGKLRDCNTHDSLLQVCD 74
                                                                       ARYHQKKEQMNEELKREAETLREREGEEFDNTCCAEKRKLWDLLEKPNSSVAAKILAII 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKRNGLINEALELTGTPEEEHMGKTTSLIESQHHHLLHCLE 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVSNFNYFYHRETDHEEQAALKEEQGNQRRESGLDTGGQRKVSCSKASFCKTGGSLESSD 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMFTFELLVRFFACPSKAEFSRNIMNIIDVVAIFPYFITLGTELAEQQPGGGGQNGQQAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSFDGILYYYQSGGRLRRPVNVSLDVFADEIRFYQ-----LGDEAMERFRE-----
                                                                                                                                                                                -FNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAFYGILPEIIGDCCY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEKGSSASKFTSIPASFWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----FVTLRVFRVFRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRDERELLRHPPVPPQPPAPAPGINGSVSGALSSGPTVAPLLP--RTLADPFFIVETTCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVFRCVLNFYRT-GKLHYPRYECISAYDDELAFYGILPEIIGDCCYEEYKDRKRENAERL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -QNQRADKRR-----AQKKARLARIRVAKTGSSNAYLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----CGTVPGSKE-----LPCGERYSVAFFCLDTACV
                                                                                                                                                                                                                                                                                                                                                                                                                              GB:M64228; NID:g200975; PIDN:AAA40112.1; PID:g200976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-Jul-1996 #text_change
ELQSLDEFGQSTDNPQLAHVEAVCIAWFTMEYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.; Salkoff,
                                                                                                                                                                                                                                                                                               258;
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                                                                                                                                                                                                                                                                                                                                 Length 857;
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A; Molecule type: mRNA
A; Residues: 1-643 < SCH>
A; Note: the clone is designated as ShD1
R; Schwarz, T.L.; Tempel, B.L.; Papazian, I
Nature 332, 740, 1988
A; Reference number: S01113
A; Contents: annotation; erratum
C; Genetics:
                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-643 < PON>
A; Cross-references: EMBL:X07132; NID:g8602; PIDN:CAA30144.1;
A; Cross-references: EMBL:X07132; NID:g8602; PIDN:CAA30144.1;
A; Note: the clone is designated as Sh-beta
R; Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan
R; Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan
Nature 331, 137-142, 1988
Nature 331, 137-142, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       potassium channel protein A (clone Sh-beta) - fruit C; Species: Drosophila melanogaster C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 C; Accession: $00480; $01111 R; Pongs, O.; Kecskemethy, N.; Mueller, R.; Krah-Jen EMBO J. 7, 1087-1096, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                   A;Cross-references: FlyBase:FBgn0003380 C;Superfamily: potassium channel protei C;Keywords: alternative splicing; trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 유
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                                                                                                                                                                                                                                                                       A;Title: Multiple potassium-channel components are produced A;Reference number: S00508; MUID:88122563; PMID:2448635 A;Accession: S01111
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Shaker encodes a family of putative potassium channel A;Reference number: S00479; MUID:88296413; PMID:2456921 A;Accession: S00480
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYLHSKRNGLLNEALELTG-----TPEEEHMGKTTSLIESQHHHLLHCLEKTTGLSYLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEWWATITWITVGYGDIYEKTLLGKIVGGLCCIAGVLVIALPIPIIVNNESEFYKEQKRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQNQRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKPVLSPESSIYTTASARTPPRSPEKHTAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FPEATRFSHSPLASLSGKSGGSTAPEVGWRGALGASGGRLMETNPIPEASRSGFFVESPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQPILNTKEMAPQSQ----PQEELEMGSMPSPVAPLPTRTEGVIDMRSMSSIDSFISCATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRLRS-----MOELSTIHIQGSEQPSLTTSRSSLNLKADD-GLRPNCKTSQITTAIISIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TRSP--SLSSHPGLTTT------CCSRRSKKTTHLPNSN------LPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KWKWTKR-----ALSETSSSKSFETKEQGSPEKARSSSSPQHLNVQQLQDMYSKMAKTQ
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21.3%;
                                                                                                                                                                                                   Papazian,
                                                                      protein
 Score
Pred.
                                                     transmembrane protein
 728; DB 2;
No. 1.8e-47;
                                                                        drk1
                                                                                                                                                                                                   D.M.; Jan, Y.N.; Jan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Krah-Jentgens,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fruit fly (Drosophila melanogaster)
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                  Length
                                                                                                                                                                                                                                                                                                                                             Jan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I.; Baumann,
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598 QTQQQLQQ--QQSHTINASAAAATSGSGSSGLT 628
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                                                                                                                                                                                                                                                                                                                             AIMPYYIGLV----------MTNNEDVSGAFV-TLRVFRVFRIFKFSRH 303
                                                                                                                                                                                                                                                                                                                                                                                                                                               ESMPSLSFRQTMWRAPENPHTSTLALVFYYVTGFFIAVSVITNVVETVP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSGGRLRRPVNVPLDVFSEEIKFYE-----LGDQAINKFRE-----DEGFIKEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RT-GKLHYPRYECISAYDDELAFYGILPEIIGDCCYEEYKDRKRENAERLMDDNDSENNQ 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERVVINVSGLRFETQLRTLNQFPDTLLGDPARRLRYFDPLRNEYFFDRSRPSFDAILYYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELIVLNVSGRRFQTWRTTLERYPDTLLGSTEKEF-FFNEDTKEYFFDRDPEVFRCVLNFY
                                                                                                                                                                                                                                                                                                AIIPYFITLATVVAEEEDTLNLPKAPVSPQDKSSNQAMSLAILRVIRLVRVFRIFKLSRH
                                                                                                                                                                                                                                                                                                                                                        TNGTKIEEDEVP---DITDPFFLIETLCIIWFTFELTVRFLACPNKLNFCRDVMNVIDII
                                                                                                                                                                                                                                     IDEOMFEONCMESSMONYPSTRSPSLSSHPGLT
                                                         AVAPFLGAQQQQQPVASSLSMSIDKQLQHPLQQLTQTQLYQQQQQQQQQQQQQQRGFKQQQQ
                                                                                                                     FNHV-----TSCPYLPGTLGQHMKKSSLSESSSDMMDLDDGVESTPGLTETHPGRS
                                                                                                                                                  KARLAR I RVAKTGSSNAYL-----HSKRNGL-----LNEALELTGTPEEEHMGKT
                                                                                                                                                                           SOGURILGYTLKSCASELGELLESLIMAIIIFATVMFYAEKGSSASKFTSIPASFWYTIV
                                                                                                                                                                                                                                                                                                                                                                                                                   RPLPDNEKORKVÁLLFÉYPESSOAARVVAIISVFVILLSIVIFCLÉTLPEFKHYKVFNTT
                                                                                                                                                                                                                                                                                                                                                                                    -CGTVPGSKELPCGERYSVAFFCLDTACVMIFTVEYLLRLFAAPSRYRFIRSVMSIIDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                       ----TSLIESQHHHLLHCLEKTTGLS-YLVDDPLLSVRTSTIKNHEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107;
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                             543
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A; Molecule type: mRNA
A; Residues: 1-512,514-564,'Q',!
A; Cross-references: GB: X06742;
                                                                                                                              A;Note: the sequence Tyr-Phe-Ile-Thr, residues 323-326, is present in R;Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y. Nature 331, 137-142, 1988
A;Title: Multiple potassium-channel components are produced by alterna A;Reference number: S00508; MUID:88122563; PMID:2448635
A;Accession: S00508
                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text change 09-Jul-2004 C;Accession: JH0193; S00508; S01110; S00479; S00482; S02822; S01674 R;Kamb, A.; Tseng-Crank, J.; Tanouye, M.A.

Neuron 1, 421-430, 1988
A;Title: Multiple products of the Drosophila Shaker gene may contribute to A;Reference number: JH0193; MUID:90166523; PMID:3272175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        potassium channel shaker form epsilon - fruit fly (Drosophila N;Alternate names: potassium channel protein A C;Species: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-656 < KAM>
                                                                                                     A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                      A; Cross-references: UNIPROT: P08510
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: JH0193
     ,565-583,'HV',
; NID:g288441;
     ,586-656 <SCH>; PIDN:CAA29917
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A;Molecule type: DNA A;Residues: 'MQMI',57,'VAG',61-452,'F',454-462,'VV',465-488,'A',490,'R',492-505,'S',507-5 ,'QL',577-579,'LQ',582-584,'QS',587,'SPHG',592-593,'MT',596-599,'LG',602-604,'LRS','TNS',

.1;

PID:g288442

A; Status: not compared with conceptual translation

A; Accession: S01110

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A;Cross-references: FlyBase:FBgn0003380

A;Introns: 61/2; 102/3; 159/1; 191/2; 256/3; 297/2; 348/3; 406/1; 449/2; 514/1

C;Superfamily: potassium channel protein drkl

C;Keywords: alternative splicing; glycoprotein; phosphoprotein; potassium channel;

F;228-246/Domain: transmembrane #status predicted <TM1>
F;279-300/Domain: transmembrane #status predicted <TM2>
F;311-332/Domain: transmembrane #status predicted <TM3>
F;358-382/Domain: S4-like region #status predicted <S4L>
F;396-417/Domain: transmembrane #status predicted <TM4>
F;432-453/Domain: transmembrane #status predicted <TM5>
F;432-453/Domain: transmembrane #status predicted <TM6>
F;437-478/Domain: transmembrane #status predicted <TM6-
F
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A; Residues: 1-452, 'F', 454-462, 'VV', 465-488, 'A', 490, 'R', 492-505, 'S', 507-510, 'A', 512, 514-5
A; Residues: 1-452, 'F', 454-462, 'VV', 465-488, 'A', 490, 'R', 492-505, 'S', 507-510, 'A', 512, 514-5
', 582-584, 'QS', 587, 'SPHG', 592-593, 'MT', 596-599, 'LG', 602-604, 'LRS', 'TNS', 640, 'QL', 643-647
A; Cross-references: EMBL:M17211; NID:g157063; PIDN:AAA28417.1; PID:g157064
A; Note: 360-Met and 464-Ile were also found
C; Comment: This protein is a component of a fast, transient, voltage-dependent, or A-type
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R;Tempel, B.L.; Papazian, D.M.; Schwarz, T.L.; Jan, Y.N.; Jan, L.Y.
Science 237, 770-775, 1987
A;Title: Sequence of a probable potassium channel component encoded at Shaker locus of D,Reference number: S01674; MUID:87292096; PMID:2441471
A;Accession: S01674
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A;Residues: 1-452,'F',454-462,'V',464-488,'A',490,'R',492-505,'S',507-510,'A',512,514-51,582-584,'QS',587,'SPHG',592-593,'MT',596-599,'LG',602-604,'LRS','TNS',640,'QL',643-647,A;Cross-references: EMBL:X07131
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A;Title: Shaker encodes a family of putative potassium channel A;Reference number: S00479; MUID:88296413; PMID:2456921
A;Accession: S00479
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A;Residues: 1-452,'F',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Ponga,
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A;Residues: 1-348,'V' <PO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: X07134;
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                                                                319
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                                                                                                                                                                                                                                      -CGTVPGSKELPCGERYSVAFFCLDTACVMIFTVEYLLRLFAAPSRYRFIRSVMSIIDVV 265
                                                                                                                                                                                                                                                                                                                             RPLPDNEKORKVWLLFEYPESSQAARVVAIISVFVILLSIVIFCLETLPEFKHYKVFNTT
SQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPASFWYTIV 363
                                                                                                                                                                                             INGTKIEEDEVP---DITDPFFLIETLCIIWFTFELTVRFLACPNKLNFCRDVMNVIDII 318
                                                                                                                                                                                                                                                                                                                                                                                              ESMPSLSFROTMWRAFENPHTSTLALVFYYVTGFFIAVSVITNVVETVP------
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31.7%;
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                                                                                                                                ---MTNNEDVSGAFV-TLRVFRVFRIFKFSRH 303
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potassium channel protein shab11 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S12746; S15058
R;Butler, A.; Wei, A.; Salkoff, L.
Nucleic Acids Res. 18, 2173-2174, 1990
A;Title: Shal, Shab, and Shaw: three genes encoding potassium channels in Dr A;Reference number: S12746; MUID:90245668; PMID:2336395
A;Accession: S12746
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A; Residues: 1-924 <BUT>
A; Cross-references: UNIPROT: P17970; EMBL: M32659
A; Cross-references: UNIPROT: P17970; EMBL: M32659
R; Butler, A.; Wei, A.; Salkoff, L.
submitted to the EMBL Data Library, March 1990
submitted to the EMBL Data Library, March 1990
A; Description: Shal, Shab, and Shaw: Three gene
A; Reference number: S15058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: FlyBase:FBgn0003383
C;Superfamily: potassium channel protein drkl
C;Keywords: ion channel; potassium channel; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-625,'YG',628-924 <BU2>
A;Cross-references: EMBL:M32659; NID:g158458;
C;Genetics:
A;Gene: shab11
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VFRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTS 353
                                                                                                                                                                                                       VTGFFIAVSVITNVVETVP-----CGTVPGSKELPCGERYSVAFFCLDTACVMIFTVEY 241
                                                                                                                                                                                                                                                                                                                                                                         YSLADNEYFFDRHPKSFSSILNFYRTGKLHIVDEMCVLAFGDDLEYWGVDELYLESCCQH
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                                                                                                                                                                                                                                                               KYHORKENVHEEMRKEAESIRORDEEEFGEGKFS--EYQKYLWELLEKPNTSFAARVIAV
                                                                                                                                                                                                                                                                                                              EYKDRK-----RENAERLMDDNDSENNQESMPSLSFRQTMWRAFENPHTSTLALVFYY 187
                                                                                                                                                                                                                                                                                                                                                                                                     FNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAFYGILPEIIGDCCYE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPFMIA-OSKAVNSRVSINVGGVRHEVLWR-TLERLPHTRLGRLGECTTHEAIVELCDD
                                                   ILRFSSSPDKWKFFKGGLNIIDLLAILFYFVSLFLLETNKNATDQFQDVRRVVQVFRIMR
                                                                                                LLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVM---TNN-----
                                                                                                                                                      ISILFİVLSTİALTLNTLPQLQHIDNGTPQDNPQLA------MVEAVCITWFTLEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 924;
                                                                                                  EDVSGAFVTLRVFR 293
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potassium channel (Kv1.5) - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-.
C;Accession: S6669
R;Sasaki, Y:, Ishii, K.; Nunoki, K.; Yamagishi, T.; Taira, N.
FEBS Lett. 372, 20-24, 1995
A;Title: The voltage-dependent K(+) channel (Kv1.5) cloned from rab.
A;Reference number: S66669; MUID:96032538; PMID:7556635
A;Reference number: S66669; MUID:96032538; PMID:7556635
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-598 <SAS>
A;Cross-references: UNIPROT:P50638; EMBL:D45025; NID:g1060972; PIDN
C;Superfamily: potassium channel protein drk1
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Matches 166; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETDHEEQAALKEEPGSQSRGTSLDAGGQRKASWSKASLCKAGGSLETADSVRRG
                               NQRADKRRA-----
                                                                          SIPASFWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQ
                                                                                                                                          RVFRIFKFSRHSQGLRILGYTLKSCASBLGFLLFSLTMAIIIFATVMFYAEKGSSASKFT
                                                                                                                                                                                CPSKAEFSRNIMNIIDIVAIFPYFITLGTELAEQQPGGGGGGQQNGQQAMSLAILRVIRLV
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                                                                                                                                                                                                                                                                                                        LPRNEFOROVWLIFEYPESSGSARAIAIVSVLVILISIITFCLETLPEFKDERELLRHPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85;
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                         QKKARLARIRVAKTGSSNAYLHSKRNG 448
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RESULT 14
A49507
A49507
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A49507; B49507
R;Attali, B.; Lesage, F.; Ziliani, P.; Guillemare, E.; Honore, E.; Waldmann.
J. Biol. Chem. 268, 24283-24289, 1993
A;Title: Multiple mRNA isoforms encoding the mouse cardiac Kv1-5 delayed rev.
A;Reference number: A49507; MUID:94043264; PMID:8226976
A;Accession: A49507
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-602 <ATT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 201-602 <AT2>
A;Cross-references: GB:L22218
C;Superfamily: potassium channel
C;Keywords: alternative splicing
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A;Accession: B49507
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                                                                                                                                                                                                                                                                                                            PSFDGILYYYQSGGRLRRPVNVSLDVFADEIRFYQ----LGDEAMERFRE-----
                                                                                                                                                                                                               SLAILRVIRLVRVPRIFKLSRHSKGLQILGKTLQASMRELGLLIFFLFIGVILFSSAVYF
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                                                                                                                                                                                                                                      ----FVTLRVFRVFRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFY
                                                                                                                                                                                                                                                                                      IMPTFELLVRFFACPSKAEFSRNIMNIIDIVAIFPYFITLGTELAEQQPGGGGQNGQQAM 383
                                                                                                                                                                                                                                                                                                                                                            FRVDRELLLHPPVPPQPPAPAPGTNASGSGVLSSGT -- TVAPLLPRTLADPFFIVETTCV
                                  EALELTGTPEEEHMGKTTSLIESQHHHLLHCLE 484
                                                                                                      IVSNFSRIYHQNQRADKRRAQKKARLARIRVA-----KTGSSNAYLHSKRNGLL--N
                                                                                                                                             AEADNQGSQLSSIPDAFWWAVVTMTTVGYGDMRPITVGGKIVGSLCAIAGVLTIALPVPV
                                                                                                                                                              AEKGSSASKFTSIPASFWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPV
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DSIRRGSCPLEKCHLKAKSNVDLRRSLYALCLD
                                                                    IVSNFNYFYHRETDHEEQAALKEEQGIQRRESGLDTGGQRKVSCSKASFH-KTGGPLEST
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Pred. No. 8.1e-47;
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potassium channel - human
C; Species: Homo sapiens (man)
C; Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004
C; Accession: 177466
R; Ramashwami, M.; Gautam, M.; Kamb, A.A.; Rudy, B.; Tanouye, M.A.; Mathew, Mol. Cell. Neurosci. 1, 214-223, 1990

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A;Title: Human potassium channel genes: molecular cloning and functional expression.
A;Reference number: I57680
A;Accession: I77466
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-499 <RES>
A;Cross-references: UNIPROT:P16389; GB:L02752; NID:g186668; PIDN:AAA36141.1; PID:g186669
C;Superfamily: potassium channel protein drk1
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Search completed: April 6, 2005, 07:17:43 Job time : 120.215 secs
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Q8hyz1 mustela put p59995 oryctolagus Q9z0v2 mus musculu Q63881 rattus norv Q9nzv8 homo sapien Q8uw33 gallus gall Q03719 mus musculu Q9nsa2 homo sapien Q95pc8 panulirus i Q95pc7 panulirus i Q95pc4 panulirus i Q95pc4 panulirus i Q95pc4 panulirus i Q95pc4 panulirus i Q95pc4 panulirus i Q95pc4 panulirus i Q95pc4 panulirus i Q95pc4 panulirus i Q95pc4 panulirus i Q95pc4 panulirus i Q95pc4 panulirus i Q95pc9 panulirus i Q95pc9 panulirus i Q95pc9 panulirus i Q95pc9 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panulirus i Q95pc3 panuli
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Q9ptd3 gallus gall
O57662 xenopus lae
Q7zw36 brachydanio
Q8hyz1 mustela put
p59995 oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9z0v1 mus musculu
Q9ttt5 oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9uk17 homo sapien
Q62897 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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45	44	43	42	41	40	39	38	37	36	<b>3</b> 5	34	33	32	
745	746	748.5	750	754.5	755.5	756	761	766.5	767	837	1103	1328.5	1654.5	
21.8	21.9	21.9	22.0	22.1	22.1	22.2	22.3	22.5	22.5	24.5	32.3	38.9	48.5	
494	858	985	911	898	911	816	911	907	908	409	236	478	372	
N	۳	<b>L</b>	ш	N	Н	N	N	ب	N	N	N	N	N	
Q91830	KCB1_RABIT	CIKB_DROME	KCB2_RABIT	Q91592	KCB2_HUMAN	Q98SV4	Q7Z7D0	KCB2_RAT	018476	P91783	Q619B6	P91784	Q75LS7	
Q9i830 oncorhynchu	. Q9mz19 oryctolagus	P17970 drosophila	Q95111 oryctolagus	Q91592 xenopus lae	Q92953 homo sapien		Q7z7d0 homo sapien	Q63099 rattus norv	018476 loligo peal	P91783 polyorchis	Q6i9b6 rattus norv	P91784 polyorchis	Q751s7 homo sapien	

## ALIGNMENTS

		RRA RRA RRA RA RA RA RA RA RA RA RA RA R		RR RR RR RR RR RR RR RR RR RR RR RR RR		Sur 23
INTERACTION WITH KCNLP2; KCNE1; KCNE2; SCN1B AND KCNAB1. MEDLINE=22233757; PubMed=12297301; DOI=10.1016/S0014-5793(02)03296-9; Deschenes I., Tomaselli G.F.; "Modulation of Kv4.3 current by accessory subunits.";	Michel U., Sauter K., Pongs O.; "Gene structures and expression profiles of three human KCND (Kv4) potassium channels mediating A-type currents I(TO) and I(SA)."; Genomics 64:144-154(2000).	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  TISSUE=Heart;  Calmels T.P.G., Faivre JF., Javre JL., Cheval B., Rouanet S.,  Bril A.;  "Long and short human isoforms of the Kv4.3 channel: cloning,  expression, electrophysiology, pharmacology and phosphorylation by  protein kinage C.".	ECIFICITY, and Heart;  SSUE=Brain, and Heart;  DLINE=99218223; PubMed=10200233;  lks D., Ling HP., Cockett M., Sokol P., Numann R.  lks D., Ling HP., Cockett M., Sokol P., Numann R.  loning and expression of the human Kv4.3 potassium  Neurophysiol. 81:1974-1977(1999).	FUNCTION.  TISSUE=Heart;  MEDLINE=99061682; PubMed=9843794;  MEDLINE=99061682; PubMed=9843794;  Kong W., Po S., Yamagishi T., Ashen M.D., Stetten G., Tomaselli G.F.;  "Isolation and characterization of the human gene encoding Ito: further diversity by alternative mRNA splicing.";  Am. J. Physiol. 275:H1963-H1970(1998).  [2]  [2]  SEQUENCE FROM N. A. (ISOEDRMS 1 AND 2). FINCTION. AND TISSUE	Name=NCND3; Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBI_TaxID=9606;  [1]  [1]  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), TISSUE SPECIFICITY, AND	T 1  HUMAN  STANDARD;  PRT; 655 AA.  KCD3 HUMAN  STANDARD;  Q9UK17; 060576; 060577; Q9UH85; Q9UH86; Q9UK16;  29-MAR-2004 (Rel. 43, Created)  29-MAR-2004 (Rel. 43, Last sequence update)  05-JUL-2004 (Rel. 44, Last annotation update)  Potassium voltage-gated channel subfamily, D member 3 (Voltage-gated potassium channel subunit Kv4.3).

```
EMBL; AF048712; AACO5121.1; -.
EMBL; AF048713; AACO5122.1; -.
EMBL; AF187963; AAF01044.1; -.
EMBL; AF187964; AAF701045.1; -.
EMBL; AF205856; AAF20924.1; -.
EMBL; AF205857; AAF20925.1; -.
EMBL; AF120491; AAD38898.1; -.
EMBL; AF166011; AAF68177.1; JOINED.
EMBL; AF166010; AAF68177.1; JOINED.
EMBL; AF166010; AAF68178.1; -.
EMBL; AF166010; AAF68178.1; -.
EMBL; AF166010; AAF68178.1; JOINED.
HSSP; Q16968; 1A68.
Genew; HGNC:6239; KCND3.
                                                                                         InterPro; IPR005821; Ion trans.
InterPro; IPR001622; K+channel pore.
InterPro; IPR001622; K+channel pore.
InterPro; IPR003091; K channel.
InterPro; IPR003091; K tetra.
InterPro; IPR003131; K tetra.
InterPro; IPR003968; KV channel.
InterPro; IPR003968; KV channel nlg.
InterPro; IPR003975; Shal_channel nlg.
InterPro; IPR003975; Shal_channel.
Pfam; PF00520; Ion_trans; 1.
Pfam; PF00520; Ion_trans; 1.
PFAM; PF00214; K tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01491; KVCHANNEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEBS
 Alternative splicing; Ion transport; Ionic channel; Potassium; Potassium channel; Potassium transport; Transport; Voltage-gated channel.

DOMAIN
1 181 Cytoplasmic (Potential)
TRANSMEM 182 202 Segment S1 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly inactivating A-type potassium channels. May contribute to I(To) current in heart and I(Sa) current in neurons. Channel properties are modulated by interactions with other alpha subunits and with regulatory subunits.
SUBUNIT: Homotetramer or heterotetramer with KCND1 and/or KCND2. Subunits with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 and KCNIP4 (By similarity). Interacts with KCNE1, KCNE2, SCNIB and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=KCND3L, Long;
IsoId=Q9UK17-1; Sequence=Displayed;
Name=2; Synonyms=KCND3S, Short;
IsoId=Q9UK17-2; Sequence=USP_008826;
TISSUE SPECIFICITY: Highly expressed in heart and brain, in particular in cortex, cerebellum, amygdala and caudate nucleus.
Detected at lower levels in liver, skeletal muscle, kidney and pancreas. Isoform 1 predominates in most tissues. Isoform 1 and isoform 2 are detected at similar levels in brain, skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and pancreas.

DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids a every third position.

SIMILARITY: Belongs to the potassium channel family. D (Shal)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Pore-forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           528:183-188 (2002)
 Cytoplasmic (Potential).
Segment S1 (Potential).
Segment S2 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    noved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
                                                                 Transmembrane;
                                                                              Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                he EMBL outst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    outstation
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                LRPNCKTSQITTAIISIPTPPALTPEGESRPPPASPGPNTNIPSITSNVVKVSVL
                                                                       GLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDG
                                                                                                          HCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMFEQNCMESSMQNYPSTRSPSLSSHP
                                                                                                                            HCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMFEQNCMESSMQNYPSTRSPSLSSHP
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                                                     GLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDG
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LRPNCKTSQITTAIISIPTPPALTPEGESRPPPPASPGPNTNIPSIASNVVKVSVL
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Selectivity filter (By similarity).
Missing (in isoform 2).
/FTId=VSP 008826.
V -> G (in Ref. 1).
P -> L (in Ref. 1).
R -> G (in Ref. 2).
E -> G (in Ref. 2).
T -> Q (in Ref. 2).
A -> D (in Ref. 2).
A -> T (in Ref. 1).
V -> A (in Ref. 3) and 4).
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Segment S3 (Potential).
Segment S4 (Potential).
Cytoplasmic (Potential).
Segment S5 (Potential).
Segment H5 (Pore-forming) (
Segment H5 (Potential).
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An W.F., E
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MEDLINE=97460452; PubMed=9314834;
Takimoto K., Li D., Hershman K.M.
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MEDLINE=96428386; PubMed=8831489;
Dixon J.E., Shi W., Wang H.-S., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potassium voltage-gated channel subfamily D m potassium channel subunit Kv4.3).
SUBCELLULAR LOCATION.
MEDLINE=22128857; Pub
Takimoto K., Yang E.-
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=Sprague-Dawley; TISSUE=Uterus;
MEDLINE=21402960; PubMed=11427525; DOI
Song M., Helguera G., Eghbali M., Zhu
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, TISSUE=Smooth muscle, and Vas deferens; MEDLINE=98111009; PubMed=9450548; DOI=10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Hippocampus;
MEDLINE=97154683; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning of a subthreshold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    correlate for the transient Circ. Res. 79:659-668(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dixon J.E., Shi W., Wang Cohen I.S., McKinnon D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
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29-MAR-2004 (Rel. 43,
05-JUL-2004 (Rel. 44,
                                                                                                         MEDLINE=20140134;
                                                                                                                                          Takimoto K., Li D., Hershman K.M., Li P., Jackson E.K., Le "Decreased expression of Kv4.2 and novel Kv4.3 K+ channel mRNAs in ventricles of renovascular hypertensive rats."; Circ. Res. 81:533-539(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serodio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96317227;
                                              Nature 403:553-556(2000)
                                                       sensors."
                                                                    Modulation
                                                                                                                                                                                                                                                            Toro L., Stefani E.;
"Remodeling of Kv4.3 potassium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Role of the Kv4.3 K+ channel in
                                                                                                                   INTERACTION WITH KCNIP1; KCNIP2 AND
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        "Molecular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Cloning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rodio P., Vega-Saenz de Miera E., Rudy B.; loning of a novel component of A-type K+ charbthreshold potentials with unique expression Neurophysiol. 75:2174-2179(1996).
                                                                                                                                                                                                                                       Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lett.
                                                                                                                                                                                                                                                                                                                                                of an A-type K+ cha
tt. 420:47-53(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g, expression and CNS distribution alpha subunit.",
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2004 (Rel. 43, Created)
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                                                                                Bowlby M.R.,
.W., Mattsson
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E
                                                                    A-type
                                                                                                                                                                                                                                      hormones.";
276:31883-31890(2001).
PubMed=12006572; DOI=10.1074/jbc.M203651200.
E.-K., Conforti L.;
                                                                                                     PubMed=10676964;
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                                                                   Betty M., Cao J., Ling K.I., Strassle B.W., T potassium channels by
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Last annotation updat
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Sciurognathi; Muridae,
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                                                                                                                                                                                                                                                                                   DOI=10.
Zhu N.,
                                                                    DOI=10.1038/35000592;
o J., Ling H.-P., Mendoza G.,
le B.W., Trimmer J.S., Rhodes
annels by a family of calcium
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Zarei M.M., Olcese R
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Murinae; Rat
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InterPro;
Pfam; PF00
Pfam; PF02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carroll K.I., Sung M.A., Betty M., Ge P., Gilbride K.J., Brown M.E., Jurman M.E., Lawson D., Silos-Santiago I., Xie Y., Covarrubias M., Rhodes K.J., Distefano P.S., An W.F.;
"Elimination of fast inactivation in Kv4 A-type potassium channels by an auxiliary subunit domain.";
Proc. Natl. Acad. Sci. U.S.A. 99:1035-1040(2002).
-!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly inactivating A-type potassium channels. May contribute to I(To) current in heart and I(Sa) current in neurons. Channel properties are modulated by interactions with other alpha subunits and with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holmqvist
Carroll K.
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J. Biol. Chem. 277:26904-26911(2002).
                                                                                                                                                     InterPro;
                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q62897-3; Sequence=VSP_008831, VSP_008832; TISSUE SPECIFICITY: Highly expressed in brain, in particular in the retrosphenial cortex, medial habenula, anterior thalamus, hippocampus, cerebellum and lateral geniculate and superior colliculus. Highly expressed in heart atrium and throughout the ventricle wall, in lung and vas deferens.

DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
SUBCELLULAR LOCATION: Integral subcellular Location: Integral subcellular control and KCN ALTERNATIVE PRODUCTS:
Event=Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulatory subunits.
SUBUNIT: Homotetrame
                                      PF00520; Ion trans; PF02214; K_tetra; 1 TS; PR00169; KCHANNEI TS; PR01518; KV43CNE
                                                                                                                                                                                                                               ; U42975; AAC52695.1; -.; U75448; AAB18337.1; -.; L48619; AAA80459.1; -.; AF334791; AAK07651.1; -.; AB003587; BAA24525.1; -.; U92897; AAB53321.1; -.; Q16968; 1A68.
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SIMILARITY: Belongs to the potassium channel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nme=1; Synonyms=Kv4.3 long
IsoId=Q62897-1; Sequence=I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q62897-2;
         PR01491;
PR01497;
                                                                                                    ; IPR003131;
; IPR004056;
; IPR003968;
; IPR005820;
; IPR003975;
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IPR001622;
IPR003091;
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            KV43CHANNEL.
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                                        GLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDG
                                                                            HCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMFEQNCMESSMQNYPSTRSPSLSSHP
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                           GLTTTCCSRRSKXTTHLENSNLPATRLRSMQELSTTHIQGSEQPSLTTSRSSLNLKADDG
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29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Potassium voltage-gated channel subfamily D me
potassium channel subunit Kv4.3).
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STRAIN-Swiss Webster; TISSUE-Heart ventricle;
Tanaka H., Janzen K., Winkfein R.J., Fiset C., Cla
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                                                                             Guo W., Li H., Aimond F., Nerbonne J.M.;
"Role of heteromultimers
                                                                                                                                                               INTERACTION WITH KCND2 AND KCNIP2.
MEDLINE=21906624; PubMed=11909823;
DOI=10.1161/01.RES.0000012664.05949.E0;
Guo W., Li H., Aimond F., Johns D.C., Rhodes
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[3]
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STRAIN=C57BL/6J; TISSUE=Diencephalon;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21481767; PubMed=11598014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60,770
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                                    outward
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420:563-573(2002).
                                                쭈
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                 generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOI=10.1093/emboj/20.20.
s R., Neuhoff H., Roeper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     828
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                                                                                                                                                                  K.J.,
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                                                                                     myocardial transient
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use heart K+
                                                                                                                                                                          Trimmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurons by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Giles W channel
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InterPro; IPR005821; Ion_trans.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR001622; K+channel.
InterPro; IPR003091; K_channel.
InterPro; IPR003131; K_tetra.
InterPro; IPR003131; K_tetra.
InterPro; IPR003968; KV_d3channel.
InterPro; IPR003968; KV_channel_nlg.
InterPro; IPR003975; Shal_channel.
InterPro; IPR003975; Shal_channel.
Pfam; PF00520; Ion_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00520; Ion trans; 1.
Pfam; PF02214; K tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01518; KV43CHANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01497; SHALCHANNEL.
                                                                                                                                                                                    TRANSMEM DOMAIN TRANSMEM
                                                                                                                                                                                                                                           TRANSMEM DOMAIN TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF107781; AAD16973.1; --
EMBL; AF107782; AAD16974.1; --
EMBL; AK033962; BAC28529.1; --
HSSP; Q16968; 1A68.
MGD; MGI:1928743; Kcnd3.
                                                                                        TRANSMEM
TRANSMEM
DOMAIN
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VARSPLIC
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                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                        Transport;
                                                                                                                                                                                                                                                                                                                                                       Alternative splicing; Ion transport; Ionic channel; Multigene family; Potassium; Potassium channel; Potassium transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified
                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isof Name=1; Synonyms=Kv4.3L; IsoId=Q9Z0V1-1; Sequence=Displayed; Name=2; Synonyms=Kv4.3M; IsoId=Q9Z0V1-2; Sequence=VSP_008827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               every third position SIMILARITY: Belongs t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: The segment S4 is probably the voltage-sensor characterized by a series of positively charged amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KCNIP4. Interacts with KCNE1, similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Homotetramer or heterotetramer with KC Associates with the regulatory subunits KCNIP1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulatory subunits. SUBUNIT: Homotetrame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Pore-forming (alpha) subunit of voltage-gated inactivating A-type potassium channels. May contribute t current in heart and I(Sa) current in neurons. Channel p are modulated by interactions with other alpha subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q9Z0V1-3; Sequence=VSP_008828, Note=May be due to intron retention. confirmation available;
                                                                                                                                                                                                                                                                                                                                   Voltage-gated
               488
               506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the potassium channel family.
                                                                                                                                                                                                                                                                                                                                          channel.
                                                                                                                                          Segment S1 (Potential).
Segment S2 (Potential).
Cytoplasmic (Potential).
Segment S3 (Potential).
Segment S4 (Potential).
Cytoplasmic (Potential).
Cytoplasmic (Potential).
Segment S5 (Potential).
Segment H5 (pore-forming)
Segment H5 (Potential).
                                                Cytoplasmic (Potential).
Selectivity filter (By similarity).
GLSYLVDDPLLSVRTSTIKNHEFIDEQMFEQNCMESSMQNY
PST -> VSSSLLPPPASSLTSQGCTHVIIPRRESSSVPFQ
SKTIVSLPLG (in isoform 3).
                                                                                                                                                                                                                                                                                                                   Cytoplasmic (Potential).
                                   FTIG=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KCNE2,
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(See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isoforms=3;
                                                                                                                                             5 (Potential).
5 (pore-forming)
6 (Potential).
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No experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KCND1 and/or KCND2.
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                                                                                                                                                                 (Potential).
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e to I(To)
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RESULT 4

RCD3 RABIT

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Matches 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                              Rae J.
                                                SEQUENCE FROM N.A.
STRAIN=New Zealand
                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                  Q9TTT5
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cornea white;

endothelium.";

(ISOFORM 1). white; TISSUE=Corneal

endothelium;

member

W

(Voltage-gated

Euteleostomi;

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29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Potassium voltage-gated channel subfamily D m
potassium channel subunit Kv4.3).
Name=KCND3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKRQDELIVLNVSGRRFQTWRTTTLER
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                                                                                                                                                                                                                                                                    LRPNCKTSQITTAIISIPTPPALTPEGESRPPPPASPGPNTNIPSITSNVVKVSVL
                                                                                                                                                                                                                                                                                                                                              GLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDG
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InterPro; IPROUJY/J, ______.

R Pfam; PF00520; Ion_trans; 1.

R Pfam; PF005214; K tetra; 1.

R Pfam; PF02214; K tetra; 1.

R Pfam; PF02214; K tetra; 1.

R Pfam; PF02214; K tetra; 1.

R PFINTS; PR0169; KCHANNEL.

DR PRINTS; PR01491; KVCHANNEL.

DR PRINTS; PR01491; KVCHANNEL.

DR PRINTS; PR01497; SHALCHANNEL.

DR PRINTS; PR01497; SHALCHANNEL.

RW Alternative splicing; Ion transport; Ionic channel; Mu

RW Alternative splicing; Ion transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transport; Transpor
 InterPro; IPR005821; Ion trans.
InterPro; IPR001622; K+channel pore.
InterPro; IPR001622; K+channel.
InterPro; IPR003091; K_channel.
InterPro; IPR003131; K_tetra.
InterPro; IPR004056; KV43channel.
InterPro; IPR003968; KV_channel.
InterPro; IPR003975; Shal_channel.
Pfam; PF00520; Ion_trans; 1.
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 TRANSMEM TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Physiol. (Lond.) 542:369-382(2002).

-!- FUNCTION: Pore-forming (alpha) sub-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF198445; AAF06021.1; -.
EMBL; AF493549; AAM46843.1; -.
HSSP; Q16968; 1A68.
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SUBUNIT: Homotetramer or heterotetramer with KCND1 and/or KCND2. Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 a KCNIP4. Interacts with KCNE1, KCNE2, SCN1B and KCNAB1 (By similarity).

SUBCELLULAR LOCATION: Integral membrane protein.

ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly inactivating A-type potassium channels. May contribute to I(To) current in heart and I(Sa) current in neurons. Channel properties are modulated by interactions with other alpha subunits and with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subfamily.
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IsoId=Q9TTT5-1; Sequence=Displayed;
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                                                             Segment S1 (Potential).
Segment S2 (Potential).
Cytoplasmic (Potential).
Segment S3 (Potential).
Segment S4 (Potential).
Cytoplasmic (Potential).
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Q8WN02;
01-MAR-2002;
01-MAR-2002;
01-OCT-2003;
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SITE
VARSPLIC
                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Voltage-gated potassium channel Kv4.3 long form.
Mustela putorius furo (Ferret).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelid
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Selectivity filter (By similarity).
Missing (in isoform 2).
/FTId=VSP_008830.
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SEQUENCE FROM N.A.
TISSUE=Heart;
MEDLINE=21896086; PubMed=11897837;
Patel S.P., Campbell D.L., Morales

Morales

м.ј.,

Strauss

Ξ

. C. ;

Mustela. NCBI\_TaxID=9669;

Vertebrata; Euteleostomi; ia; Mustelidae; Mustelinae

Mustelinae;

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RESULT
Q9PTD3
ID Q9
AC Q9
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REMBL; AF454388; AAL51038.1; -.

RESP; Q63881; 1S6C.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0008076; C:voltage-gated potassium channel con

GO; GO:0005515; F:protein binding; IEA.

GO; GO:0005249; F:voltage-gated potassium channel act

GO; GO:0005249; F:voltage-gated potassium channel act

GO; GO:0006812; P:cation transport; IEA.

GO; GO:0006813; P:potassium ion transport; IEA.

Pfam; PF00520; Ion trans; 1.

Pfam; PF02214; K tetra; 1.

PRINTS; PR01518; KV43CHANNEL.

PRINTS; PR01491; KVCHANNEL.

PRINTS; PR01491; KVCHANNEL.

PRINTS; PR01491; KVCHANNEL.

SMART; SM00225; BTB; I.
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Best Local (
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                     PRELIMINARY;
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AA; 73375 MW; 3DD3E94819FEF6C1 CRC64;
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Best Local S
Matches 624
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GO; GO:0008076; C:voltage-gated potassium channel complex;

RR GO; GO:0005515; F:protein binding; IEA.

GO; GO:0005249; F:voltage-gated potassium channel activity;

RR GO; GO:0006812; P:cation transport; IEA.

GO; GO:0006813; P:potassium ion transport; IEA.

RR GO; GO:0006813; P:potassium ion transport; IEA.

RR InterPro; IPR000210; BTB POZ.

RR InterPro; IPR001622; K+channel pore.

InterPro; IPR003968; Kv channel.

InterPro; IPR003968; Kv channel.

InterPro; IPR003968; Kv channel.

InterPro; IPR003968; Kv channel.

RR InterPro; IPR0039131; K ctannel.

RR InterPro; IPR003131; K ctannel.

RR InterPro; IPR003975; Shal channel.

RR FAINTS; PR001516; KVCHANNEL.

RR PRINTS; PR001491; KVCHANNEL.

RR PRINTS; PR01497; SHALCHANNEL.

RR PRINTS; PR01497; SHALCHANNEL.

RR PRINTS; PR01497; SHALCHANNEL.

RR PRINTS; PR01497; SHALCHANNEL.

RR SMART; SM00225; BTB; 1.

InterPro; IOnic Channel; Transmembrane; Transport.

SCOUENCE 658 AA; 73896 MW; OF8743D4AF8B12A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF209722;
HSSP; Q63881; 18
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STRAIN=breed W
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01-MAY-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Potassium channel Kv4.3.
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                                                                                                                     FSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPASFW
                                                                                                                                                                                         EYLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGAFVTLRVFRVFRIFK
                                                                                                                                                                                                                                                                                                                   TLALVFYYVTGFFIAVSVITNVVETVPCGTVPGSKELPCGERYSVAFFCLDTACVMIFTV
                                                                                            FSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPASFW
                                                                                                                                                                                                                                                                                        TLALVFYYVIGFFIAVSVITNVVETVPCGTVPGNKELPCGERYAVAFFCLDTACVMIFTV
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Pred. No. 1.5e-194;
9; Mismatches 12;
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                                                          Query Match
Best Local S
Matches 573
                                                                                                                  InterPro; IPR003975; Shal channel.
Pfam; PF00520; Ion_trans; 1.
Pfam; PF02214; K tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01518; KV43CHANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01497; SHALCHANNEL.
SMART; SM00225; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 057662;
057662;
01-JUN-1998
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Lautermilch N.J., Spitzer N.C.;

Submitted (FEB-1997) to the EMBL/GenBank/DDBJ

EMBL; U89265; AAB94379.1; -.

HSSP; Q63881; 186C.
                                                                                                                                                                                                                                                                                                                                                                     Potassium channel xKv4.3.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
                                                                                           PROSITE; PS50097;
Ion transport; Ion
SEQUENCE 659 AA;
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
                                                          Local Sim
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                          <u>بــ</u>
                                                                   Similarity
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                        DGLRPNCKAAQITTAIISIPTPPALTPEGESRPPPSSPGHSTNISTTTTSNVVKVSVL
        YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF
                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                           Ionic channel; Transmembrane; Transport.
AA; 74515 MW; 73F5CF339C6A0F47 CRC64;
                                                                                                             BTB;
85.7%;
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                                                        Score 2925; DB 2; Lo
Pred. No. 5.7e-175;
-- wismatches 40;
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ia; Pipoidea;
                                                                                                                                                                                                                                                                                                                               databases
                                                                         Length
                                                                                                                                                                                                                                                                            activity; IEA
                                                           Indels
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                                                                            659;
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                                                           Gaps
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC STRAIN=AB; TISSUE=Whole body;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Paher, T. Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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01-JUN-2003 (TrEMBLrel. 2
01-JUN-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
Potassium voltage-gated c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPA
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24, Last sequence update)
25, Last annotation update)
channel, Shal-related family,
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Best Loc
Matches
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Pfam; PF02214; K tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01518; KV43CHANNEL
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01497; SHALCHANNEL
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                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00225; BTB; 1.
Ion transport; Ionic channel; Transmembrane; Transport.
SEQUENCE 638 AA; 72053 MW; 038645FB28947F47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR005821; Ion trans.
InterPro; IPR001622; K+channel pore.
InterPro; IPR004056; KV43channel.
InterPro; IPR003968; Kv channel.
InterPro; IPR003991; K channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
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InterPro; IPR005820; M+channel_nlg.
InterPro; IPR003975; Shal_channel.
Pfam; PF00520; Ion_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WHEL; BCO45304; AAH45304.1; -.

ISSP; Q63881; 1S6C.

ZFIN; ZDB-GENE-030131-5626; zgc:55306.

30; GO:0016021; C:integral to membrane; IEA.

30; GO:0008076; C:voltage-gated potassium channel cor

30; GO:0005515; F:protein binding; IEA.

30; GO:0005249; F:voltage-gated potassium channel act

30; GO:0006812; P:cation transport; IEA.

30; GO:0006813; P:potassium ion transport; IEA.
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             TIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQNQRADKRR 420
                                            SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSSASKFTSIPASFWY
                                                                                         YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYBCISAYDDELAF
                                                                                                                                                                                           FGIIPEIISDCCYEEYKORKRENTERLMDDLE
 LMIVIT
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Pred. No. 8.8e
71; Mismatches
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                                                                                                                                                                                                                                                                                                                                   5; DB 2;
d.8e-153;
58;
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                                                   Query Match
Best Local S
Matches 488
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ
EMBL; AY147192; AAN39878.1; -.
HSSP; Q63881; 1S6C.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0008076; C:voltage-gated potassium chan
GO; GO:0005515; F:protein binding; IEA.
GO; GO:0005249; F:voltage-gated potassium chan
GO; GO:0005249; F:voltage-gated potassium chan
GO; GO:0006812; P:cation transport; IEA.
GO; GO:0006813; P:potassium ion transport; IEA.
GO; GO:0006813; P:potassium ion transport; IEA.
InterPro; IPR000210; BTB POZ.
InterPro; IPR00122; K-channel pore.
InterPro; IPR00125; KV42channel.
InterPro; IPR003968; KV_channel.
InterPro; IPR003131; K_tetra.
InterPro; IPR003131; K_tetra.
InterPro; IPR003131; K_tetra.
InterPro; IPR005820; M+channel nlg.
                                                                                                                                         Pfam; PF00520; Ion trans; 1.
Pfam; PF02214; K tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01517; KV42CHANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01497; SHALCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Voltage-gated potassium channel Kv4.2.
Mustela putorius furo (Ferret).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Butanalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8HYZ1;
Q8HYZ1;
01-MAR-2003
                                                                                                      SMART; SM00225; BTB; 1.

Ion transport; Ionic channel; Transmembrane; Transport SEQUENCE 630 AA; 70565 MW; DA4CFD16998A9842 CRC64;
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                                                                 Similarity
                 MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKR-QDELIVLNVSGRRFQTWRTTLE
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   MAAGVAAWLPFARAAAIGWMPVASGPMPAPPRQERKRTQDALIVLNVSGTRFQTWQDTLE
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                                                    Conservative
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                                                              73.6%;
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Shal_channel.
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                                                                Score 2510.5;
Pred. No. 5e-
                                                   Mismatches
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                                                   Indels
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                                                                           Length
                                                                             630;
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29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Potassium voltage-gated channel subfamily D m
potassium channel subunit Kv4.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=New Rae J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=KCND2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _TaxID=9986;
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InterPro; IPR001622; K+channel_pore.
InterPro; IPR003131; K_tetra.
InterPro; IPR005820; M+channel_nlg.
Pfam; PP00520; Ion_trans; 1.
Pfam; PP02214; K_tetra; 1.
Ion transport; Ionic channel; Multigene fa Potassium; Potassium channel; Potassium transport; Voltage-gated channel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulatory subunits.

SUBUNIT: Homotetramer or heterotetramer with KCND1 and/o Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP4. Interacts with DPP6, DLG4 and FREQ. Interacts wi and FLNC (By similarity).

I SUBCELULAR LOCATION: Integral membrane protein.

I TISSUE SPECIFICITY: Detected in brain frontal cortex.

I DOMAIN: The segment S4 is probably the voltage-sensor an characterized by a series of positively charged amino accevry third position.

PTM: Phosphorylated on serine and threonine residues (By
                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
SIMILARITY: Belongs to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are modulated by interactions with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                          1 MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKR-QDELIVLNVSGRRFQTWRTTLE
                                                                                                                                                                               Similarity
                    STLALVFYYVTGFFIAVSVITNVVETVPCGTVPGS-KBLPCGERYSVAFFCLDTACVMIF
                                                                                                                    MAAGVAAWLPFARAAAIGWMPVASGPMPAPPRQERKRTQDALIVLNVSGTRFQTWQDTLE
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                                                                                                                                                                              73.48;
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                                                                                                                                                                  69;
                                                                                                                                                                                                                           Cytoplasmic (Potential).
Selectivity filter (By similarity).
Phosphothreonine (By similarity).
Phosphoserine (By similarity).
Phosphothreonine (By similarity).
Phosphothreonine (By similarity).
Phosphothreonine (By similarity).
Phosphoterine (By similarity).
E -> K (in Ref. 2).
K -> R (in Ref. 2).
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                                                                                                                                                                                                                                                                                                                                     Segment S1 (Potential).
Segment S2 (Potential).
Cytoplasmic (Potential).
Segment S3 (Potential).
Segment S4 (Potential).
Cytoplasmic (Potential).
Segment S5 (Potential).
Segment S6 (Potential).
Segment H5 (Pore-forming) (Segment S6 (Potential).
                                                                                                                                                                              Score 2504.5;
Pred. No. 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probably the voltage-sensor of positively charged amino
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                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                    (Potential).
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"Isolation of full-length" (JUN-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Swiss Webster; TISSUE-Heart ventricle; Tanaka H., Janzen K., Winkfein R.J., Fiset C., Clark R.B., "Cloning and functional characterization of mouse heart K+ alpha subunits, Kv1.5, Kv4.2 and Kv4.3."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KCD2 MOUSE STANDARD; PRT; 630 AA. Q9ZOVZ; Q8BSK3; Q8CHB7; Q9JJ60; 29-MAR-2004 (Rel. 43, Created) 29-MAR-2004 (Rel. 43, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T., Ohara O., Koga H.;
Ohara O., Koga H.;
"Prediction of the coding sequences of mouse homologues of KIAA gene:
I. The complete nucleotide sequences of 100 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potassium voltage-gated channel subfamily D potassium channel subunit Kv4.2). Name=Kcnd2; Synonyms=Kiaal044;
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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
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RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
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RA Maglott D.R., Maltais L., Marchiomni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
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RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
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RA Hira A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
PA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
PA Yasunishi A., Yashiraki Y.,
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"Role of heteromultimers
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21906624; PubMed=11909823;
DOI=10.1161/01.RES.0000012664.05949.E0;
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SUBCELLULAR LOCATION: Integral membrane TISSUE SPECIFICITY: Detected in brain, e medial habenular nucleus, striatum, amyg cerebellum.

DOMAIN: The segment S4 is probably the v characterized by a series of positively
                                                                                                                                               regulatory subunits.
SUBUNIT: Homotetramer or heterotetramer with KCND1 and/or KCND3. Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 a KCNIP4. Interacts with DPP6, DLG4 and FREQ. Interacts with FLNA
                                                                                                                                                                                                                         FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly inactivating A-type potassium channels. May contribute to I(To) current in heart and I(Sa) current in neurons. Channel properties are modulated by interactions with other alpha subunits and with
                                                                                                                                                                                                                                                                                                       K+ currents.";
es. 90:586-593(2002).
                                                                                                                           FLNC (By similarity)
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9:179-188(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR005821; Ion trans.

InterPro; IPR001622; K+channel pore.

InterPro; IPR003091; K_channel.

InterPro; IPR003091; K_tetra.

InterPro; IPR0030968; KV_channel.

InterPro; IPR0030968; KV_channel.

InterPro; IPR003975; Shal_channel.

InterPro; IPR003975; Shal_channel.

Pfam; PF00520; Ion_trans; 1.

Pfam; PF00520; Ion_trans; 1.

Pfam; PF02214; K_tetra; 1.

Pfam; PF02214; K_tetra; 1.

PFINTS; PR0169; KCHANNEL.

PRINTS; PR0169; KCHANNEL.

PRINTS; PR01491; KV42CHANNEL.

PRINTS; PR01491; KV42CHANNEL.

PRINTS; PR01491; KV42CHANNEL.

PRINTS; PR01491; KV42CHANNEL.

PRINTS; PR01497; SHALCHANNEL.

POTABSSium; Potassium channel; Multigene family; Phosph

Potassium; Potassium channel; Potassium transport; Tra

DOMAIN

1 183 Cytoplasmic (Potential).
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EMBL; AB045326; BAA97986.1; ALT_FRAME.
EMBL; AB093280; BAC41464.1; ALT_INIT.
EMBL; AK032268; BAC27787.1; -.
EMBL; AK032772; BAC28015.1; -.
PIR; PT0675; PT0675.
HSSP; Q16968; 1A68.
MGD; MGI:102663; Kcnd2.
InterPro; IPR005821; Ion_trans.
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CAUTION: Ref
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MAAGVAAWLFFARAAAIGWMPVANCPMPLAPADKNKR-QDELIVLNVSGRRFQTWRTTLE
                                                MAAGVAAWLPFARAAAIGWMPVASGPMPAPPRQERKRTQDALIVLNVSGTRFQTWQDTLE
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630 AA;
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Segment S2 (Potential).
Cytoplasmic (Potential).
Segment S3 (Potential).
Segment S4 (Potential).
Cytoplasmic (Potential).
Cytoplasmic (Potential).
Segment S5 (Potential).
Segment H5 (pore-forming)
Segment H5 (pore-forming)
Segment H5 (Potential).
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Phosphoserine.
Phosphothreonine.
Phosphothreonine.
                                                                                                Score 2503.5; DB 1;
Pred. No. 1.4e-148;
8; Mismatches 70;
                                                                                                                                               S->A: Abolishes PKA-mediated of channel activity.
V -> A (in Ref. 2).
S -> R (in Ref. 3).
; 7FB94277429E7683 CRC64;
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(pore-forming)
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RESULT 12

KCD2_RAT

ID KCD2
AC Q388

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C Q63881; Q00090; Q99249;

C Q63881; Q00090; Q99249;

T 29-MAR-2004 (Rel. 43, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

Potassium voltage-gated channel subfamily D member 2 (

Potassium channel subunit Kv4.2) (Shall) (RK5).
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Neuron 7:471-483(1991).

Neuron 7:471-483(1991).

N [2]

P SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

SEQUENCE FROM N.A., AND TISSUE=Heart;

C STRAIN=Sprague-Dawley; TISSUE=Heart;

REDLINE=91156694; PubMed=1705709;

XX MEDLINE=91156694; PubMed=1705709;
                                                                                 Roberds S.L., Tamkun M.M.;
Roberds S.L., Tamkun M.M.;
"Cloning and tissue-specific expression of five very potassium channel cDNAs expressed in rat heart.";
proc. Natl. Acad. Sci. U.S.A. 88:1798-1802(1991).
                                                                                                                                                                                                                                         TISSUE=Hippocampus;
MEDLINE=92000693; PubMed=1840649; DOI=10.1
Baldwin T.J., Tsaur M.-L., Lopez G.A., Jan
"Characterization of a mammalian cDNA for
sensitive K+ channel.";
Neuron 7:471-483(1991).
INTERACTION WITH KCNIP1; KCNIP2 AND KCNIP3.
MEDLINE=20140134; PubMed=10676964; DOI=10.1038/35000592;
An W.F., Bowlby M.R., Betty M., Cao J., Ling H.-P., Mend
Hinson J.W., Mattsson K.I., Strassle B.W., Trimmer J.S.,
                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.,
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G.A., Jan Y.N., Jan L.Y.;
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 Ling H.-P., Mendoza
N., Trimmer J.S., Rho
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EMBL;
                                                                   This SWISS-PROT entry is copyright. It is produced through a centre of the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22464931; PubMed=12575952; DOI=10.1016/S0896-6273(02)01185-6; Nadal M.S., Ozaita A., Amarillo Y., Vega-Saenz de Miera E., Ma Y., Mo W., Goldberg E.M., Misumi Y., Ikehara Y., Neubert T.A., Rudy B.; "The CD26-related dipeptidyl aminopeptidase-like protein DPPX is a critical component of neuronal A-type K+ channels."; Neuron 37:449-461(2003).
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MEDLINE=22037905; PubMed=11923279; DOI=10.1074/jbc.M109412200;
Wong W., Newell E.W., Jugloff D.G.M., Jones O.T., Schlichter L
"Cell surface targeting and clustering interactions between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21964093; PubMed=11847232; DOI=10.1074/jbc.M200897200; Morohashi Y., Hatano N., Ohya S., Takikawa R., Watabiki T., Takasugi N., Imaizumi Y., Tomita T., Iwatsubo T.; Takasugi N., Imaizumi Y., Tomita T., Iwatsubo T.; "Molecular cloning and characterization of CALP/KChIP4, a nove hand protein interacting with presenilin 2 and voltage-gated p
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MEDLINE=21532927; PubMed=11606724; DOI=10.1073/pnas.221168498;
Nakamura T.Y., Pountney D.J., Ozaita A., Nandi S., Ueda S., Ru
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPP6, DLG4 or FREQ may increase cell surface expression.
TISSUE SPECIFICITY: Highly expressed in heart and througout the brain, with similar levels in cortex and hypothalamus, and much higher levels in hippocampus, dentate gyrus and the habenular nucleus of the thalamus. Detected at similar levels in heart atrium and ventricle. Detected in aorta, cardiac and smooth
                                                                                                                                                                                                                                                                                                                                                        similarity).
SIMILARITY: Belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Homotetramer or heterotetramer with KCND1 and/or KCND3. Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 a KCNIP4. Interacts with FLNA and FLNC (By similarity). Interacts with DPP6, DLG4 and FREQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly inactivating A-type potassium channels. May contribute to I(To) current in heart and I(Sa) current in neurons. Channel properties are modulated by interactions with other alpha subunits and with
                                                                                                                                                                                                                                                                                                                                                                                                                                                               characterized
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S64320;
M59980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  third position.
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                                                                                                                                                                                                                                                                                                           Ref.2 sequence
AAB19939.1;
AAA40929.1;
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Matches 486
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InterPro; IPR001622; K+channel pore
InterPro; IPR003091; K channel.
InterPro; IPR003131; K tetra.
InterPro; IPR004055; KV42channel.
InterPro; IPR003968; Kv channel.
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Pfam; PF02214; K tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01517; KV42CHANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01497; SHALCHANNEL.
3D-structure; Ion_transport; Ic
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KRRAQKKARLARIRVAKTGSSNAYLHSKRNGLLNEALELTGTPEEEHMGKTTSLIESQHH
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; M+channel_nlg.
; Shal_channel.
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Voltage-gated channel
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Selectivity filter (By similarity).
Phosphothreonine (By similarity).
Phosphothreonine (By similarity).
Phosphothreonine (By similarity).
Phosphothreonine (By similarity).
Phosphothreonine (By similarity).
Phosphoserine (By similarity).
Missing: Abolishes interaction with
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Segment S2 (Potential).
Segment S2 (Potential).
Segment S3 (Potential).
Segment S4 (Potential).
Segment S4 (Potential).
Segment S5 (Potential).
Segment S6 (Potential).
Segment H5 (pore-forming)
Segment S6 (Potential).
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Pred. No. 2.4e-148;
9; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic
Segment S1 (
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KCD2 HUMAN

STANDARD;

PRT;

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Q9NZV8;

O95012;

O95021;

Q9UBY7;

Q9UN98;

Q9UNH9;

29-MAR-2004 (Rel. 43, Created)

29-MAR-2004 (Rel. 43, Last sequence update)

05-JUL-2004 (Rel. 44, Last annotation update)

Potassium voltage-gated channel subfamily D member 2

potassium channel subunit KV4.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., FUNCTION, AND 113555 C. ----- TISSUE=Brain cortex;

MEDLINE=20195625; PubMed=10729221; DOI=10.1006/geno.2000.6117;

MEDLINE=20195625; PubMed=10729221; DOI=10.1006/geno.2000.6117;
                          MEDLINE 22616434; PubMed=12690205; DOI=10.1126/science.1083423; Scherer S.W., Cheung J., MacDonald J.R., Osborne L.R., Nakabayas Herbrick J.-A., Carson A.R., Parker-Katiraee L., Skaug J., Khaja Zhang J., Hudek A.K., Li M., Haddad M., Duggan G.E., Fernandez E Kanematsu E., Gentles S., Christopoulos C.C., Choufani S., Kwasnicka D., Zheng X.H., Lai Z., Nusskern D., Zhang Q., Gu Z., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Zhuman C., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Zhuman C., Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Zhuman C.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99397452; PubMed=10470851;
Kikuno R., Nagase T., Ishikawa K.-I., Hirosawa M., Miyajima Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human ge The complete sequences of 100 new cDNA clones from brain whifor large proteins in vitro.";
DNA Res. 6:197-205(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND FUNCTION.
MEDLINE=20017432; PubMed=10551270;
Zhu X.-R., Wulf A., Schwarz M., Isbrandt D., Pongs O.;
"Characterization of human Kv4.2 mediating a rapidly-inactivating transient voltage-sensitive K+ current.";
Recept. Channels 6:387-400(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The for DNA
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Kong W., Po S., Yamagishi T., Ashen M.D., Stetten "Isolation and characterization of the human gene further diversity by alternative mRNA splicing."; Am. J. Physiol. 275:H1963-H1970(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                            "Gene structures and expression profiles of three human KCND (Kv4) potassium channels mediating A-type currents I(TO) and I(SA).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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., Sauter K., Pongs O.;
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      lowaczyk M.J.,
Zackai E.H.,
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Primates;
      Grebe
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      Cox S.
   D., Shuman C.,
Kirkpatrick S.J.,
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                                                                                                                                                  , Nakabayashi K.
g J., Khaja R.,
Fernandez B.A.,
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Rahman N., Friedman J.M., Heng H.H.Q., Pelicci P.G., Lo-Coco F. Belloni E., Shaffer L.G., Pober B., Morton C.C., Gusella J.F., Bruns G.A.P., Korf B.R., Quade B.J., Ligon A.H., Ferguson H., Higgins A.W., Leach N.T., Herrick S.R., Lemyre E., Farra C.G., Kim H.-G., Summers A.M., Gripp K.W., Roberts W., Szatmari P., Winsor E.J.T., Grzeschik K.-H., Teebi A., Minassian B.A., Kere Armengol L., Pujana M.A., Estivill X., Wilson M.D., Koop B.F., Tosi S., Moore G.E., Boright A.P., Zlotorynski E., Kerem B., Kroisel P.M., Petek E., Oscier D.G., Mould S.J., Doehner H., Doehner K., Rommens J.M., Vincent J.B., Venter J.C., Li P.W., Mural R.J., Adams M.D., Tsui L.-C.; "Human chromosome 7: DNA sequence and biology.";
                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. They use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Homotetramer or heterotetramer with KCND1 and/or KCND3. Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 a KCNIP4. Interacts with DP6, DLG4 and FREQ (By similarity). Interacts with FLNA and FLNC.

SUBCELLULAR LOCATION: Integral membrane protein. Detected in dendrites in cultured hippocampal neurons.

TISSUE SPECIFICITY: Highly expressed throughout the brain. Expression is very low or absent in other tissues.

DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
SIMILARITY:
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other alpha
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Q16968; 11
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AC004946;
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AB028967; BAA82996.2; ALT_INT
AJ010969; CAB56841.1; -.
AF166008; AAF65618.1; -.
AF166007; AAF65618.1; JOINED.
PR00169;
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| IPR003131;
| IPR004055;
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PR01491;
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SHPGLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKA
                        HLLHCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMFEQNCMESSMQNYPSTRSPSLS
                                                       KRRAQKKARLARIRVAKTGSSNAYLHSKRNGLLNEALELTGTPEEEHMGKTTSLIESQHH
                                                                                                                       FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPAS
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Selectivity filter (By similarity).
Phosphothreonine (By similarity).
Phosphoserine (By similarity).
Phosphothreonine (By similarity).
Phosphothreonine (By similarity).
Phosphoserine (By similarity).
Phosphoserine (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Segment S1 (Potential).
Segment S2 (Potential).
Cytoplasmic (Potential).
Segment S3 (Potential).
Segment S4 (Potential).
Cytoplasmic (Potential).
Segment S5 (Potential).
Segment H5 (pore-forming)
Segment H5 (Potential).
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FLNC.
N -> S (in R
Q -> P (in R
Q -> R (in R
Q -> R (in R
Q -> V (in R
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Pred. No. 2.8e-148;
9; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                       N -> S (in Ref. 1).
Q -> P (in Ref. 1).
Q -> R (in Ref. 1).
Q -> R (in Ref. 1).
I -> V (in Ref. 1).
OC11E62FFA220421 C
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transport;
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Sakai Y., Sokolowski B.H.A.;

Sakai Y., Sokolowski B.H.A.;

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

REMBL; AF075160; AAL56633.1; -.

REMBL; AF075160; AL56633.1; -.

REMBL; AF075160; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0008076; C:voltage-gated potassium channel complex;

REMGO; GO:0005219; F:voltage-gated potassium channel activity

REMGO; GO:0006812; P:cation transport; IEA.

GO; GO:0006813; P:potassium ion transport; IEA.

REMGO; GO:001691; Kv42CHANNEL.

REMGO; FRO11517; KV42CHANNEL.

REMGO; FRO11517; KV42CHANNEL.

REMGO; GO:0006813; P:potassium ion transport; IEA.

REMGO; GO:0005214; K_tetra; 1.

REMGO; GO:0006813; P:potassium channel activity

REMGO; GO:0006813; P:potassium ion transport; IEA.

REMGO;
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Best Local 9
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Q8UW33;
Q8UW33;
Q1-MAR-2002 (TrEMBLrel. 2
Q1-MAR-2002 (TrEMBLrel. 2
Q1-MAR-2004 (TrEMBLrel. 2
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Eukaryota; Metazoa; Chordata;
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shal-like voltage-gated
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B9; Conservative
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                                                                                                                                                                                                                                                                                                                           STLALVFYYVTGFFIAVSVITNVVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF
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FWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQNQRAD
                                                                                         FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPAS
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74.0%;
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20, Last s
26, Last a
l potassium
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; Pred. No. 3.3e-148;
62; Mismatches 75;
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A Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
A Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
A Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
A Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
A Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
A Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
A Garimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
A Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
A Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
A Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
A Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
A Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
A Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
A Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
A Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
A Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
A Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
A Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
A Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
A Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
A Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
A Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
A Petrovsky N., Pillai R., Pontius P., Setou M., Shimada K.,
A Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
A Walla R., Pontius P., Vanagisawa M., Yang I., Yang I.,
A Petrovsky N., Pillai R., Pontius P., Pontius P.,
A Petrovsky N., Pillai R., Pontius P.,
A Petrovsky N., Pillai R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potassium voltage-gated che potassium channel subunit Name-Kcnd1;
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Q03719; Q8CC68;
29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence up
05-JUL-2004 (Rel. 44, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 145-647 FROM N.A. STRAIN=C57BL/6J; TISSUE=Epididymis; MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91239573; PubMed=2034678; Pak M.D., Baker K., Covarrubias M.,
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MGD; MGI:96671; Kcndl.

InterPro; IPR005821; Ion_trans.
InterPro; IPR001622; K+channel pore.
InterPro; IPR003091; K_channel.
InterPro; IPR003191; K_tetra.
InterPro; IPR003191; K_tetra.
InterPro; IPR004054; KV41channel.
InterPro; IPR003978; KV2channel nlg.
InterPro; IPR003978; Shallchannel.
InterPro; IPR003975; Shallchannel.
                                                                                                                                                                                                                                    Pfam; PF00520; Ion trans; 1.
Pfam; PF02214; K tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01516; KV41CHANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01497; SHALCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subfamily members, Kv4.1 and Kv4.2.";
FEBS Lett. 499:205-209(2001).
-!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated rainactivating A-type potassium channels. May contribute to current in the heart and I(Sa) current in neurons. Channel properties are modulated by subunit assembly.
-!- SUBUNIT: Homotetramer or heterotetramer with KCND2 and/or
                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Different effects of the Ca(2+)-binding subfamily members, Kv4.1 and Kv4.2."; FEBS Lett. 499:205-209(2001).
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Nakamura T.Y., Na
Coetzee W.A.;
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Yasunishi A., Yoshino M., Waterston R.,
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Voltage-gated
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Potassium channel; Potassium
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SIMILARITY: Belongs to the notation.
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Segment S1 (Potential).
Segment S2 (Potential).
Cytoplasmic (Potential).
Cytoplasmic (Potential).
Segment S4 (Potential).
Segment S4 (Potential).
Cytoplasmic (Potential).
Segment S5 (Potential).
Segment H5 (Pore-forming).
Segment H5 (Potential).
Segment S6 (Potential).
Segment S6 (Potential).
Segment S7 (Potential).
Segment S8 (Potential).
Segment S9 (Potential).
Segment S9 (Potential).
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Transmembrane;
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KCNIP1, KCNIP2,
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RADKRRAQKVRLARIRLAKSGTTNAFLQYKQNG----GLEDSGSGDGQMLCVRSRSAFE 475
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Compugen Ltd
Aaw79585 Human Kv4
Aaw79589 Human Kv4
Abb79584 Human Kv4
Aaw79590 Human Kv
Adf91398 Wild-type
Adw79591 Human Kv
Add48188 Rat Prote
Ads16294 Human Vol
Aab86321 Human Vol
Aab86321 Human O64
Min10929 Human O64
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	ADJ25645	œ	149	22.5	746	45
Abb67198 Drosophil	ABB67198	4.	1019	22.5	747	44
Abb57774 Drosophil	ABB57774	4.	985	22.6	749	43
Adi38328 Human cat	ADI38328	œ	858	22.6	750	42
Aao17058 Human KCN	AA017058	ហ	858	22.6	750	41
Aay32015 Human cat	AAY32015	N	858	22.6	750	40
. Adj79874 CIKA_huma	ADJ79874	7	854	22.6	750	39
Abp58354 Human pot	ABP58354	თ	854	22.6	750	38
Adi30143 Drosophil	ADI30143	œ	985	22.8	758	37
Adi30147 Drosophil	ADI30147	œ	985	22.8	758	36
Adj69676 Human hea	ADJ69676	7	911	23.1	766	35
Adj79875 CIKA_huma	ADJ79875	7	806	23.3	774.5	34
Adm43517 Human ova	ADM43517	œ	255	25.4	844.5	33
Adj11256 Human ova	ADJ11256	œ	255	25.4	844.5	32
.Adm10926 Human O64	ADM10926	7	255	25.4	844.5	31
Aay13524 Amino aci	AAY13524	N	214	26.2	869	30
Aab86320 Human Kv4	AAB86320	4	217	26.9	894	29
Abb71722 Drosophil	ABB71722	4	571	58.9	1955	28
Aay34123 Human pot	AAY34123	N	646	63.9	2121.5	27
Aab86318 Human Kv4	AAB86318	4	646	64.1	2127.5	26

## ALIGNMENTS

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WPI; 200
N-PSDB;
                                                                                                                        New isolated polynucleotide encoding human Kv4.3 potassium channel polypeptide, useful as probe in a diagnostic method for detecting acid encoding human Kv4.3, and for treating Alzheimer's and heart
                                                                                                                                                                                                                                                                                                        Kv4.3; potassium channel; human; Alzheimer's disease; heart disease;
nootropic; neuroprotective; cardiant; gene therapy.
                                                                                                                  diseases.
                                                                                                                                                                                   Cockett MI,
                                                                                                                                                                                                                                                       28-MAY-2002
                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  ABB79585 standard;
                                                                                                                                                                                                                     23-OCT-1998;
                                                                                                                                                                                                                                     23-OCT-1998;
                                                                                                                                                                                                                                                                       US6395477-B1.
                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                Human Kv4.3 potassium channel (short form).
                                                                                                                                                                                                                                                                                                                                                                  ABB79585;
                                                                                                                                                                                                    (AMHP ) AMERICAN HOME PROD CORP.
                                                                                                                                                          2002-556093/59.
DB; ABN84401.
                                                                                                                                                                                   Dilks DW,
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                                                                                                                                                                                                                                                                                                                                                                                 protein;
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                                                                                                                                                                                    Sokol
                                                                                                                                 nucleic
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The present sequence is the protein sequence of the short isoform of novel human potassium channel Kv4.3. 2 Isoforms of human Kv4.3 have been identified: a full-length form (hKv4.3 long) (see ABB79584); and the short form, which has a deletion of 19 amino acids in the carboxy domain after the predicted sixth transmembrane domain (hKv4.3 short). Human heart primarily expresses hKv4.3 long, whereas human brain contains both forms. The invention provides Kv4.3 polypeptides, polynucleotides, and methods for producing these polynucleotides. The Kv4.3 polypeptides and polynucleotides are useful in the diagnosis, treatment and screening of human diseases relating to an excess or deficiency of hKv4.3 activity, including Alzheimer's disease and heart disease

Claim 1; Col 23-26; 19pp; English.

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RESULT 2
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AC AAW7
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                           01-OCT-1998.
                                           W09842833-A2
                                                           Homo sapiens
                                                                                    Potassium channel; Kv; hKv4.3;
                                                                                                      Human
                                                                                                                       11-JAN-1999
                                                                                                                                                         AAW79589
          23-MAR-1998;
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                                                                                                     Kv potassium channel hKv4.3 (shorter isoform).
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                                                                                                                                                       standard; protein; 636
                                                                                                                                                                                                             PPALTPEGESRPPPASPGPNTNIPSITSNVVKVSVL
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Pred. No. 1.6e-313;
0; Mismatches 0;
                                                                                    human; Alzheimer's disease; arrhythmia;
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channel hKv4.3. The sequence was deduced from an isolated hKv4.3.

CC polynucleotide (see AAV61571), and has 99% identity with rat Kv4.3.

CC Hydrophobicity analysis indicates 6 transmembrane domains, typical of all CC KV family related proteins. A longer isoform (see AAW79590) has been CC identified, which has an additional 19 amino acids inserted between amino CC acids 487 and 488. The invention relates to hKv4.3 polypeptides and CC polynucleotides, and to methods for producing such polypeptides by recombinant techniques. hKv4.3 polypeptides can be used to identify CC agonists and antagonists of hKv4.3 polypeptides can be used to identify CC claimed are methods for utilising such agonists and antagonists for the treatment of subjects in need of enhanced or reduced activity or expression of hKv4.3 polypeptide. These include the treatment of cardiac arrhythmias and Alzheimer's disease. The invention can also be used to detect disease associated with inappropriate hKv4.3 expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-1997;
09-DEC-1997;
11-DEC-1997;
Sequence 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the amino acid sequence for an isoform of human Kv potassium channel hKv4.3. The sequence was deduced from an isolated hKv4.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New potassium channel polypeptides, hKv4.3 poly:nucleotide(s) useful in the treatment arrhythmias and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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97EP-00402971.
97EP-00403007.
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Query Match
Best Local Similarity
Matches .634; Conserv Conservative 99.7%; 0; Score 3311; DB 2; Pred. No. 1.2e-312; 0; Mismatches 2; Length Indels 636; 0; Gaps

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                                                     AQKKARLARIRVAKTGSSNAYLHSKRNGLLNEALELTGTPEEEHMGKTTSLIESQHHHLL
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Matches 636
                                                                                                                                                    The present sequence is the protein sequence of the long isoform of novel human potassium channel Kv4.3. 2 Isoforms of human Kv4.3 have been identified: the present full-length form (hKv4.3 long); and a second form (see ABB79585), which has a deletion of 19 amino acids in the carboxy domain after the predicted sixth transmembrane domain (hKv4.3 short). Human heart primarily expresses hKv4.3 long, whereas human brain contains both forms. The invention provides Kv4.3 polypeptides, polynucleotides, and methods for producing these polynucleotides. The Kv4.3 polypeptides and polynucleotides are useful in the diagnosis, treatment and screening of human diseases relating to an excess or deficiency of hKv4.3 activity, including Alzheimer's disease and heart disease
                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide encoding human Kv4.3 potassium channel polypeptide, useful as probe in a diagnostic method for detecting acid encoding human Kv4.3, and for treating Alzheimer's and heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kv4.3; potassium channel; human; Alzheimer's disease; heart
nootropic; neuroprotective; cardiant; gene therapy.
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                                                                                                                                 Sequence
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N-PSDB;
               AAV61572
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New potassium channel polypeptides, hKv4.3 poly:nucleotide(s) useful in the treatment arrhythmias and Alzheimer's disease. and hKv4.3-encoding of disorders including cardiac

2; Page 26-27; 47pp; English

This is the amino acid sequence for an isoform of human Kv potassium channel hKv4.3. The sequence was deduced from an isolated hKv4.3 polynucleotide (see AAV61572), and has 97% identity with rat Kv4.3. Kydrophobicity analysis indicates 6 transmembrane domains, typical of all Kv4rophobicity analysis indicates 6 transmembrane domains, typical of all Kv4ramily related proteins. A shorter isoform (see AAW79589) has been cidentified, which lacks amino acid residues 488-506 of the longer cisoform. The invention relates to hKv4.3 polypeptides and polynucleotides, and to methods for producing such polypeptides by recombinant techniques. hKv4.3 polypeptides can be used to identify agonists and antagonists of hKv4.3 and to raise specific antibodies. Also claimed are methods for utilising such agonists and antagonists for the treatment of subjects in need of enhanced or reduced activity or expression of hKv4.3 polypeptide. These include the treatment of cardiac arrhythmias and Alzheimer's disease. The invention can also be used to to detect disease associated with inappropriate hKv4.3 expression or Also a11 ç

Sequence 655 AA;

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                                                   GLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDG
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밁 601 LRPNCKTSQITTAIISIPTPPALTPEGESRPPPASPGPNTNIPSIASNVVKVSAL 655

standard; protein; 655 ጅ

tranquiliser; sedative; neuroprotective; nootropic; antiparkinsonian; nematode worm; voltage-gated potassium channel; Kv4; agonist; antagonist; blocker; pharmaceutical; agrochemical; veterinary; arrhythmia; tachycardia; congestive heart failure; epilepsy; stroke; traumatic brain injury; anxiety; insomnia; Alzheimer's disease; Wild-type hKv4.3 Parkinson's disease Antiarrhythmic; 26-FEB-2004 (first cardiovascular; anticonvulsant; #SEQ entry) IJ ū cerebroprotective;

Homo sapiens.

WO2003097682-A1.

27-NOV-2003

14-MAY-2003; 2003WO-IB002453.

15-MAY-2002; 2002GB-00011123. 15-MAY-2002; 2002US-0378076P. 15-MAY-2002; 2002US-0378131P.

(DEVG-) DEVGEN 3

Kaletta TJ, Dewulf NE,

New nematode worm expressing a heterologous nucleotide sequence encoding a functional voltage-gated potassium channel of the Kv4 family, useful for determining compounds that interact with the voltage-gated potassium

1; **SEQ** ID NO ა •• 82pp; English.

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AC The invention relates to a nematode worm that expresses a heterologous nucleotide sequence encoding a functional voltage-gated potassium channel of the Kv4 family, or its analog, mutant, variant, homolog, ortholog, part or fragment. The nematode worm is useful in determining whether a compound interacts with the voltage-gated potassium channel of the Kv4 family or whether a compound is an agonist, antagonist, opener and/or blocker of the voltage-gated potassium channel expressed by the nematode worm. The methods are used for identifying and developing compounds that interact with voltage-gated potassium channels of the Kv4 family. The compounds may be used in the development and/or preparation of compositions for pharmaceutical, agrochemical and/or veterinary use. These may be used in preparing compositions for preventing or treating cliseases or conditions such as arrhythmia, tachycardia, congestive heart failure, epilepsy, stroke, traumatic brain injury, anxiety, insomnia, and the contract of the current sequence or arrivation of the current sequence. represents wild-type

Sequence 655 AA;

ঠ Query Match
Best Local Similarity
Matches 634; Conser MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKRQDELIVLNVSGRRFQTWRTTLER 99.1%; 0 Score Pred. Mismatches 3291.5; DB No. 1e-310; 2 8 Indels Length 19; Gaps 60

MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKRQDELIVLNVSGRRFQTWRTTLER

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09-DEC-1997;
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                             Calmels TPG,
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97EP-00402971.
97EP-00403007.
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                                               BEECHAM LAB
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New potassium channel polypeptides, hKv4.3 poly:nucleotide(s) useful in the treatment arrhythmias and Alzheimer's disease.

    and hKv4.3-encoding
of disorders including

                                                                                                                          cardiac
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English.

This is the amino acid sequence for an isoform of human Kv potassium CC channel hKv4.3. The sequence was deduced from an isolated hKv4.3 CC channel hKv4.3. The sequence was deduced from an isolated hKv4.3 CC polynucleotide (see AAV61573), and has 98% identity with rat Kv4.3. CC Hydrophobicity analysis indicates 6 transmembrane domains, typical of all CC KV family related proteins. hKv4.3 isoforms (see AAW79589 and AAW79590) CC are also claimed. The invention relates to hKv4.3 polypeptides and CC polynucleotides, and to methods for producing such polypeptides by recombinant techniques. hKv4.3 polypeptides can be used to identify CC agonists and antagonists of hKv4.3 polypeptides can be used to identify CC claimed are methods for utilising such agonists and antagonists for the treatment of subjects in need of enhanced or reduced activity or CC expression of hKv4.3 polypeptide. These include the treatment of cardiac arrhythmias and Alzheimer's disease. The invention can also be used to to detect disease associated with inappropriate hKv4.3 expression or Also

Sequence 636 A,

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                             SNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDGLRPNCKTSQITTAIISIPT
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                                                The invention discloses a composition comprising two or more isolated rat CC or human polynucleotides or a polynucleotide which represents a fragment, CC derivative or allelic variation of the nucleic acid sequence. Also Cc claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating colypeptides or their antibodies. The polynucleotide given in the specification, a method for identifying a compound useful in treating pain (e.g. spinal segmental nerve injury (CNung), chronic construction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (described in Table 3 of the specification, but was obtained in electronic form directly from WIPO at ftp. wipo.int/pub/sublished_pct_sequences.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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GENBANK; AAB53321.
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nic constriction injury; CCI; spared nerve injury; SNI; Chung.
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Query Match Best Local Similarity

98.98;

Score 3284.5; DB 7; Pred. No. 4.8e-310;

Length 655;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening drug candidates that target voltage dependent ion channel protein, involves contacting screening protein with chemical compound, which is drug candidate and determining whether chemical compound binds to screening protein.
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                                                    This invention describes a novel potassium channel protein (I) that is either human Kv4.1 or Kv4.2. Eukaryotic cells that express potassium channels containing (I) are used to identify and test: (i) compounds for treatment of neurodegenerative diseases (autism, epilepsy, ischemia, stroke; Alzheimer's, Parkinson's and Huntington's diseases) or cardiac arrhythmia, or those that improve learning capacity and memory; and (ii) activators of protein kinases. Host cells that express (I) can identify agents that do not interact significantly with channels and control I to (a quickly activated transient current), so lack the side effects of known anti-arrhythmic agents. They also eliminate, or reduce, the need for testing on organ cultures
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Kv4.1; potassium channel protein; Kv4.2; autism; epilepsy; neurodegenerative disease; ischemia; stroke; Alzheimer's disease; Parkinson's disease; Huntington's disease; cardiac arrhythmia; memory; learning capacity; protein kinase activator; anti-arrhythmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New potassium channel subunit proteins, useful for identifying and testing potential pharmaceuticals, e.g. anti-arrhythmic or neurologicals.
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01-NOV-2001;
26-NOV-2001;
                                                                                                                                                                                                                                                            Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                 14-AUG-2002;
                                                                                                                                                                                                                          Rattus norvegicus
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2001US-0333347P.
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Claim New composition comprising two or more isolated polypeptides, preparing a medicament for treating pain in an animal. invention discloses a composition comprising two or more isolated rat 2003-268312/26. ANK; AAA80459. 1; Page; 1017pp; BAYER ĀG Á Befort English ζ, Costigan 3

useful

cor human polynucleotides or a polynucleotide which represents a fragment, correct derivative or allelic variation of the nucleic acid sequence. Also colaimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a cell cubic to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal cell cubic expressed in an animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more cell composition, a method for identifying a compound useful in treating cell composition, a method for identifying a compound useful in treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene cellication) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed cellication, but was obtained in electronic form directly from WIPO at the composition and animal of or the composition of the printed cellication and part of the printed cellication and control of the printed cellication and control of the printed cellication and cellication of the cellication at the cellication of the cellication at the cellication of the cellication at the cellication of the cellication at the cellication of the cellication at the cellication of the cellication at the cellication of the cellication at the cellication ftp.wipo.int/pub/published\_pct\_sequences

Sequence 611 A,

Similarity

92.0%;

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Length 611;

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03-APR-2001;
02-OCT-2001;
02-AUG-2002;
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01-MAY-2000;
15-AUG-2000;
07-SEP-2000;
                                                 This invention describes a novel ovarian tumour protein which can be uto detecting the presence of an ovarian cancer in a patient by stimulating and/or expanding T cells specific for the tumour protein. products of the invention can also be used in a method to inhibit the development of a cancer in a patient comprising (a) incubating CP4+ and/or CD8+ T cells isolated from a patient with at least one ovarian tumour protein, such that T cell proliferate and (b) administering to patient the proliferated T cells. The cytostatic polynucleotides or polypeptides described in the invention are useful for treating or inhibiting the development of cancer, particularly ovarian cancer and stimulating and/or expanding T cells specific for a tumour protein or
                                                                                                                                                                                                        New polynucleotides encoding tumor proteins, treating or inhibiting the development of cancer, particularly ovarian cancer, and for stimulating and/or expanding T cells specific for a tumor protein.
                      Sequence 630
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2000US-00561778.
2000US-00640173.
2000US-00656668.
2000US-00713550.
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2002US-00212677.
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Matches 486; Conserv
10-SEP-1999;
01-MAY-2000;
15-AUG-2000;
07-SEP-2000;
                                                                                                                                    ovarian; tumour protein; cancer;
cytostatic; gene therapy; human;
                                                    05-FEB-2003;
                                                                                            US2003206918-A1
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                                                                          06-NOV-2003
                                                                                                                                                                      Human
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- 99US-00394374.
2000US-00561778.
2000US-00640173.
2000US-00656668.
                                                    2003US-00361811.
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Matches 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-NOV-2000; 2000US-00713550.
03-APR-2001; 2001US-00825294.
02-OCT-2001; 2001US-00970966.
02-AUG-2002; 2002US-00212677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides encoding tumor proteins, treating development of cancer, particularly ovarian cancer, and/or expanding T cells specific for a tumor prote
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HLLHCLEKTTNHEFVDEQVFEESCMEVATVNRPSSHSPSLSSQQGVTSTCCSRRHKKTFR
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Pred. No. 2e-2
69; Mismatches
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.2e-235;
.70;
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                                                    SSEDEQAFVSKSGSSFETQHH
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                                Query Match
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15-AUG-2000; 2000US-00640173.

07-SEP-2000; 2000US-00656668.

14-NOV-2000; 2000US-00713550.

03-APR-2001; 2001US-00825294.

02-OCT-2001; 2001US-00970966.

02-AUG-2002; 2002US-00212677.
                                                                                                                                                                                to detecting the presence of an ovarian cancer in a patient by stimulating and/or expanding T cells specific for the tumour protein. products of the invention can also be used in a method to inhibit the development of a cancer in a patient comprising (a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one ovarian tumour protein, such that T cell proliferate and (b) administering to patient the proliferated T cells. The cytostatic polynucleotides or polypeptides described in the invention are useful for treating or inhibiting the development of cancer, particularly ovarian cancer and stimulating and/or expanding T cells specific for a tumour protein or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding tumor proteins, treating or development of cancer, particularly ovarian cancer, and f and/or expanding T cells specific for a tumor protein.
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                                                                                                                   ovarian; tumour protein; cancer;
cytostatic; gene therapy; human;
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     99US-00394374.

2000US-00561778.

2000US-00640173.

2000US-00656668.

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2001US-00825294.

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This invention describes a novel ovarian tumour protein which can be u to detecting the presence of an ovarian cancer in a patient by stimulating and/or expanding T cells specific for the tumour protein. products of the invention can also be used in a method to inhibit the development of a cancer in a patient comprising (a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one ovarian tumour protein, such that T cell proliferate and (b) administering to patient the proliferated T cells. The cytostatic polynucleotides or polypeptides described in the invention are useful for treating or inhibiting the development of cancer, particularly ovarian cancer and stimulating and/or expanding T cells specific for a tumour protein or gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides encoding tumor proteins, treating or inhibiting the development of cancer, particularly ovarian cancer, and for stimulating and/or expanding T cells specific for a tumor protein.
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15-AUG-2000; 2000US-00640173.
07-SEP-2000; 2000US-00656668.
14-NOV-2000; 2000US-00713550.
03-APR-2001; 2001US-00825294.
02-OCT-2001; 2001US-00970966.
02-AUG-2002; 2002US-00361811.
                                                                                                                                                                                                                                                                                                                                          This invention relates to novel isolated polynucleotides and methods for the therapy and diagnosis of cancer, particularly ovarian cancer. Specifically, it refers to these polynucleotides and the encoded polypeptides thereof, as well as immunogenic peptides, antibodies, antigen presenting cells (APCs) and immune system cells (e.g. T cells) that are targeted to those cells expressing the proteins of interest. The present invention describes methods that are useful for stimulating and/ or expanding T cells specific for a tumourigenic protein (i.e. T cell therapy). Furthermore, compositions can be used for the diagnosis, treatment and/ or prevention of ovarian cancer by stimulating an immune response in a patient. Accordingly, these compositions exhibit cytostatic activity. This polypeptide is a human ovarian tumour antigen protein sequence given in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated ovarian tumor polynucleotide encoding ovarian tumor polypeptide, useful as probes of primers for detecting presence of cancer in a patient.
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                                                                                                                                                                                                                                                                                          Sequence
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Sequence 5, Appli	Sequence 9, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 17, Appl	Sequence 1, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 18, Appl	Sequence 10288, A	Sequence 8, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 7, Appli	Sequence 7475, Ap	Sequence 9860, Ap	Sequence 12, Appl	Sequence 6, Appli

## ALIGNMENTS

US-09-178-109-4

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Sequence 4, Application US/09178109
; Patent No. 6395477
; GENERAL INFORMATION:
    APPLICANT: Cockett, Mark I.
    APPLICANT: Dilks, Daniel W.
    APPLICANT: Dilks, Daniel W.
    APPLICANT: Sokol, Patricia T.
    TITLE OF INVENTION: Human Potassium Channel Polynucleotides and TITLE OF INVENTION: Polypeptides and Uses Therefor FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/09/178,109
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
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TYPE: PRT
ORGANISM: human
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GENERAL INFORMATION:

APPLICANT: Antoine Michel Alain Bril
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-François Simon Pierre Faivre
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rouanet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1998-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR APPLICATION NUMBER: US 97402971.2
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-09
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 636
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US-09-142-791A-2
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ORGANISM: HOMO
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; Patent No. 6395477
; GENERAL INFORMATION:
APPLICANT: Cockett, Mark I.
APPLICANT: Dilks, Daniel W.
APPLICANT: Chang Ling, Huai-Ping
APPLICANT: Sokol, Patricia T.
TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
TITLE OF INVENTION: Polypeptides and Uses Therefor
FILE REFERENCE: ahp-98089
CURRENT APPLICATION NUMBER: US/09/178,109
CURRENT FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 655
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; TYPE: PRT
; ORGANISM: human
US-09-178-109-2
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CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR FILING DATE: 1998-03-23
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR FILING DATE: 1997-12-09
PRIOR FILING DATE: 1997-12-11
NUMBER: FASTSEQ for Windows Version 3.0
SOFTWARE: FASTSEQ for Windows Version 3.0
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; TYPE: PRT
; ORGANISM: HOMO S
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APPLICANT: Antoine Michel Alain Bril
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Faivre
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rouanet
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                                                                                                                                                                                                           Matches
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Best Local :
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TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
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                                          YGILPEIIGDCCYEEYKDRKRENAERLMDUNDSENNQESMPSLSFRQTMWRAFENPHTST
                                                            YGILPEIIGDCCYEEYKDRKRENAERLMDDNDSENNQESMPSLSFRQTMWRAFENPHTST 180
                                                                                                YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF
                                                                                                                YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF
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                                                                                                                                                                                                       Score 3291.5; DB 3
Pred. No. 6.6e-307;
0; Mismatches 2;
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APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Thierry Paul Gerard Calmels
APPLICANT: Jean-Francois Simon Pierre Faivre
APPLICANT: Jean-Luc Javre
APPLICANT: Sabine Rouanet
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30012
CURRENT APPLICATION NUMBER: US/09/142,791A
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: PCT/EP98/01901
PRIOR APPLICATION NUMBER: UK 9706377.0
PRIOR APPLICATION NUMBER: US 9706377.0
PRIOR APPLICATION NUMBER: EP 97402971.2
PRIOR APPLICATION NUMBER: EP 97403007.4
PRIOR FILING DATE: 1997-12-09
PRIOR FILING DATE: 1997-12-11
                                                                                                                                                                                                                                      ; SOFTWARE: FASTSEQ f
; SEQ ID NO 6
; LENGTH: 636
; TYPE: PRT
; ORGANISM: HOMO SAF
US-09-142-791A-6
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US-09-142-791A-6
                                                                                                                                                    Query Match
Best Local Similarity
Matches 630; Conserv
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Patent No. 6368823
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                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows
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                       61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF 120
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nilarity 99.1%;
Conservative
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                                                                                                                                                         Score 3285; DB 3;
Pred. No. 2.6e-306;
1; Mismatches 5;
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                                                                                                                                                                                                Length 636;
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Sequence 6828, Application US/09949016;
Patent No. 6812339;
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CL001307;
CURRENT APPLICATION NUMBER: US/09/949,016;
CURRENT FILING DATE: 2000-04-14;
PRIOR APPLICATION NUMBER: 60/241,755;
PRIOR APPLICATION NUMBER: 60/237,768;
PRIOR APPLICATION NUMBER: 60/237,768;
PRIOR FILING DATE: 2000-10-03;
PRIOR APPLICATION NUMBER: 60/231,498;
PRIOR APPLICATION NUMBER: 60/231,498;
PRIOR FILING DATE: 2000-09-08;
NUMBER OF SEQ ID NOS: 207012;
SOFTWARE: FASTSEQ for Windows Version 4.0;
SEQ ID NO 6828;
LENGTH: 630
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                                                                                                             Query Match
Best Local Similarity
Matches 486; Conserv
                                                                                                                                                                    TYPE: PRT
ORGANISM: Human
-09-949-016-6828
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                                                                                                             Conservative
                                                                                                           75.8%; Score 2518; DB 4; ]
75.8%; Pred. No. 1.2e-232;
tive 69; Mismatches 70;
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GENERAL INCOMPATION:
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Muller, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761el Human Potassium Cha
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR APPLICATION NUMBER: FCT/US99/03826
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: FOT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 646
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                                                           TYPE: PRT

ORGANISM: H. sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(646)
OTHER INFORMATION: Xaa =
US-09-336-643A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09336643A Patent No. 6399761
Query Match
Best Local Similarity
Matches 428; Conserv
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63.9%; ilarity 65.1%; Conservative 7
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; Score 2121.5; DB 3; 
; Pred. No. 1.5e-194; 
78; Mismatches 116;
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                          Length
                              646;
 35;
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239 607

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Sequence 8327, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8327

LENGTH: 260

TYPE: PRT
ORGANISM: Human
US-09-949-016-8327
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US-09-949-016-8327
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      26.1%;
    Score
Pred.
    865.5; DB 4;
No. 1.4e-74;
                                                                                                                                                                                                                                                                                                                                                               ASSOCIATED OF DETECTION AND USES THEREOF
                       Length
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APPLICANT: ICAgen, Inc.
TITLE OF INVENTION: Kv10.1, a No. 6727353el
TITLE OF INVENTION: Human Brain
FILE REFERENCE: 018512-005910US
CURRENT APPLICATION NUMBER: US/09/833,466
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/197,793
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 806
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
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Best Local Similarity
Matches 220; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                            ARYHOKKEOMNEELRREAETMRDGEGEEFDNTCCPDK--RKKLWDLLEKPNSSVAAKILA
                                                                                                                                                                                                                                             EEYKORK-----RENAERLMDDNDSENNQESMPSLSFRQTMWRAFENPHTSTLALVFY
YVTGFFIAVSVITNVVETVP-----CGTVPGSKELPCGERYSVAFFCLDTACVMIFTV
                                                                                                                                                                                                                                                                                   DYNLNENEYFFDRHPGAFTSILNFYRTGKLHMMEEMCALSFGQELDYWGIDEIYLESCCQ
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                                                           EYLLRELSSPNKWKFFKGPLNVIDLLAILPYYVTIFLTESNKSVLQFQNVRRVVQIFRIM
                                                                                            EYLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNN-----EDVSGAFVTLRVF 292
                                                                                                                                                                                                                                                                                                                  -FNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAFYGILPEIIGDCCY 133
                                                                                                                                                                                                                                                                                                                                                                 LPPEPVDIIRSKTCSRRVKINVGGLNHEVLWR-TLDRLPRTRLGKLRDCNTHESLLEVCD
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                                                                                                                                  IVSILFIVESTIALSENTEPELQETDEFGQLNDNRQLA------HVEAVCIAWFTM
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                                                                                                                                                                                                                                                                                                                                                                                                                                        23.3%; Score 774.5; DB 4; ilarity 27.7%; Pred. No. 4.7e-65; Conservative 116; Mismatches 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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APPLICANT: Jegla, Timothy James
APPLICANT: ICAgen, Inc.
TITLE OF INVENTION: Kv10.1, a No. 6727353el
TITLE OF INVENTION: Human Brain
FILE REFERENCE: 018512-005910US
CURRENT APPLICATION NUMBER: US/09/833,466
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/197,793
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 854
                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens; FEATURE:
OTHER INFORMATION: human voltage-gated potassium channel Kv2.1
US-09-833-466-12
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US-09-833-466-12
                                                                                                                                                                                                                Best Loca
Matches
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                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                               27 MPLAPAD--KNKRQDELIVLNVSGRRFQT-WRTTLERYPDTLLG-----STEKEFF----
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                  EEYKDRKRENAERLMDDNDSENNQE-----SMPSLSFRQTMWRAFENPHTSTLALVFYYV
                                                                                              -FNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAFYGILPEIIGDCCY 133
                                                                                                                                       LPPEPMEIVRSKACSRRVRLNVGGLAHEVLWR-TLDRLPRTRLGKLRDCNTHDSLLEVCD
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                                                          DYSLDDNEYFFDRHPGAFTSILNFYRTGRLHMMEEMCALSFSQELDYWGIDEIYLESCCQ
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                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                18; Score 750; DB 4; Length 854;
28; Pred. No. 1.2e-62;
1114; Mismatches 220; Indels 124;
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                                                                                                                                       70
                                                                                                                                                                             74
                                                                                                                                                                                                                                                                                        APPLICANT: The Rockefeller University
FITLE OF INVENTION: Assays for Screening Compounds Which Interact With
FITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Catio
FITLE OF INVENTION: Channel Proteins, and Uses Thereof
FILE REFERENCE: 018512-002901US
CURRENT APPLICATION NUMBER: US/09/275,252A
CURRENT FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: US 09/045,529
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 09/054,347
PRIOR APPLICATION NUMBER: US 09/054,347
PRIOR APPLICATION NUMBER: WO PCT/US99/06307
PRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 858
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                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo
US-09-275-252A-6
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Patent No. 6641997
                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MacKinnon, APPLICANT: The Rocke
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                                     -FNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAFYGILPEIIGDCCY 133
                                                                             LPPEPMEIVRSKACSRRVRLNVGGLAHEVLWR-TLDRLPRTRLGKLRDCNTHDSLLEVCD
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   DYSLODNEYFFORHPGAFTSILNFYRTGRLHMMEEMCALSFSQELDYWGIDEIYLESCCQ
                                                                                                                                                           Conservative
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29.2%; Pred. No. 1.2e-62;
ative 114; Mismatches 220;
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RESULT 12
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                                FILING DATE: June 5,1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08449
FILING DATE: 28 JUL 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INC
TELEPHONE: 201-994-1744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: ROSELAND
STATE: NEW JERSEY
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                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: MacKinnon, Roderick
APPLICANT: The Rockefeller Un
                                SOFTWARE: PatentIn Ver. SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09275252A Patent No. 6641997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 172; Conserv
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                                                                                                                                                                     APPLICANT: The Rockefeller University
TITLE OF INVENTION: Assays for Screening Compounds Which Interact
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic C
TITLE OF INVENTION: Channel Proteins, and Uses Thereof
FILE REFERENCE: 018512-002901US
CURRENT APPLICATION NUMBER: US/09/275,252A
CURRENT FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: US 09/045,529
PRIOR FILING DATE: 1998-03-20
                                                                       PRIOR APPLICATION NUMBER: US 09/054,347
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: WO PCT/US99/06307
PRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 42
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SEQUENCE CHARACTERISTICS:
LENGTH: 539 AMINO ACIDS
TYPE: AMINO ACID
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TOPOLOGY: LIN
MOLECULE TYPE:
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RESULT 14

US-09-949-016-8164

Sequence 8164, Application US/09949016

Patent NO. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20
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                                                                                  ; ORGANISM: Human
US-09-949-016-8164
                                                                                                                      PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 8164
LENGTH: 552
TYPE: PRT
Query Match 21.7%;
Best Local Similarity 31.2%;
Matches 176; Conservative 10
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%; Score 719; DB 4; Length 552;
%; Pred. No. 5.5e-60;
105; Mismatches 172; Indels 1
   Indels 112;
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6195
LENGTH: 523
TYPE: PRT
ORGANISM: Human
US-09-949-016-6195
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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                                                                                            Matches
                                                                                                                               Query Match
Best Local
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                                                                                            21.6%; Score 718; DB 4; I ilarity 31.2%; Pred. No. 6.3e-60; Conservative 105; Mismatches 172;
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Search Job ti	B 8	gb - Qy	dg VQ	g 49	g 99	B 8	B 8	B 8	g Q	DЬ
Search completed: April 6, 2005, 07:21:30 Job time : 106.44 secs	517 LSSHPGLTTTCCSRRSKKTTHLPNS 541    :   :     :	457 TGTPEEEHMGKTTSLIESQHHHLLHCLEKTTNHEFIDEQMFEQNCMESSMQNYPSTRSPS 516 : :	397 LPVPVIVSNFSRIYHQNQRADKRRAQKKARLARIRVAKTGSSNAYLHSKRNGLLNEALEL 456         : ::: ;  :  ;   ;   ;   ;   ;	337 TVMFYAEKGSSASKETSIPASFWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIA 396 : :::	278 NNEDVSGAFV-TLRVFRVFRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFA 336 :	225 AFFCLDTACVMIETVEYLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMT 277      ::   :   :	185 FYYVTGFFIAVSVITNVVETVPCGTVPGSKELPCGERYSV 224	125 PEIIGDCCYEEYKDRKRENAERLMDDNDSENNQESMPSLSFRQTMWRAFENPHTSTLALV 184	67 GSTEKEF-FFNEDTKEYFFDRDPEVPRCVLNFYRT-GKLHYPRYECISAYDDELAFYGIL 124   :: : :      :   : :: ::  : ::   79 GDPKRRMRYFDPLRNEYFFDRNRPSFDAILYYYQSGGRIRRPVNVPIDIFSEEIRFYQ 136	19 GAPPQGGCGGGGCDRYEPLPPSLPAAGEQDCCGERVVINISGVRFETQLKTLCQFPETLL 78
:30			QKKARLARIRVAKTGSSNAYLHSKRNGLLNEALEL 456 :  :  :   ;   ;   456			SRYRFIRSVMSIIDVVAIMPYYIGLVMT 277  :    :: ::  :  :    	VPGSKELPCYSV 224	DNDSENNQESMPSLSFRQTMWRAFENPHTSTLALV 184 :    ::              EGFLREEERPLPRRDFQRQVWLLFEYPESSGPARG 183	FRCVLNFYRT-GKLHYPRYECISAYDDELAFYGIL 124	AGEQDCCGERVVINISGVRFETQLKTLCQFPETLL 78

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Minimum DB
Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                     Score
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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US-10-377-139-6
US-10-212-677-259
US-10-212-677-260
US-10-212-677-261
US-10-361-811-259
US-10-361-811-250
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US-10-361-811-261
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Sequence 4, Appli
Sequence 2, Appli
Sequence 25, Appli
Sequence 259, App
Sequence 260, App
Sequence 261, App
Sequence 258, App
Sequence 259, App
Sequence 261, App
Sequence 261, App
Sequence 261, App
Sequence 258, App
Sequence 259, App
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## ALIGNMENTS

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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 636
TYPE: PRT
ORGANISM: human
US-10-062-879-4
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Best Local Similarity
Matches 636; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: ahp-98089
CURRENT APPLICATION NUMBER: US/10/062,879
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US/09/178,109
PRIOR FILING DATE: 1998-10-23
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APPLICANT: Dilks, Daniel W.
APPLICANT: Chang Ling, Huai-Ping
APPLICANT: Sokol, Patricia T.
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                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                        61 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF 120
13
                                                                                                                 1 MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKRQDELIVLNVSGRRFQTWRTTLER
                                                                                            1 MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKRQDELIVLNVSGRRFQTWRTTLER
                                                                                                                                                                               100.0%; Score 3320; DB 13; Length 636; ilarity 100.0%; Pred. No. 1.4e-278; Conservative 0; Mismatches 0; Indels 0;
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180

300

300 240 240

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Sequence 2, Application US/10062879; Publication No. US20020127649A1; GENERAL INFORMATION:
APPLICANT: Cockett, Mark I.
APPLICANT: Dilks, Daniel W.
APPLICANT: Chang Ling, Huai-Ping;
APPLICANT: Sokol, Patricia T.
TITLE OF INVENTION: Human Potassium Channel Polynucleotides and TITLE OF INVENTION: Polypeptides and Uses Therefor; FILE REFERENCE: ahp-98089; CURRENT APPLICATION NUMBER: US/10/062,879; CURRENT FILING DATE: 2002-01-31; PRIOR APPLICATION NUMBER: US/09/178,109; PRIOR FILING DATE: 1998-10-23; NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0; LENGTH: 655
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Best Local Similarity 97.1%;
Matches 636; Conservative
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ORGANISM: human
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                                                                        MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKRQDELIVLNVSGRRFQTWRTTLER
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                                 YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF
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                  YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF
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                                                                                                                                  Score 3300.5; DB 13; Length Pred. No. 7.3e-277; O; Mismatches O; Indels
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Publication No. US20040175761A1
GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo
-10-377-139-6
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                                                                                                                                                                               Local Similarity
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YGILPEIIGDCCYEEYKDRKRENAERLMDDNDSENNQESMPSLSFRQTMWRAFENPHTST
                                                             YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF
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                                                                                                                                                                  Conservative
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2.2e-275;
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480 420 420 360 360

480

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Gaps

180

120

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GENERAL INFORMATION:

APPLICANT: Chenault, Ruth A.

APPLICANT: Xu, Jiangchun

APPLICANT: Fanger, Gary R.

APPLICANT: Harlocker, Susan L.

APPLICANT: MCNeill, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.484C7

CURRENT APPLICATION NUMBER: US/10/212,677

CURRENT APPLICATION NUMBER: US/10/212,677

CURRENT FILING DATE: 2002-08-02

NUMBER OF SEQ ID NOS: 288

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 258

LENGTH: 630

TYPE: PRT

ORGANISM: Homo sapiens

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Best Local Similarity 75.8%;
Matches 486; Conservative 6
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                                                                 RYPDTLLGSTEKEFFFNEDTKEYFFDRDFEVFRCVLNFYRTGKLHYPRYECISAYDDELA
                                                                                                      MAAGVAAWLPFARAAAIGWMPVASGPMPAPPRQERKRTQDALIVLNVSGTRFQTWQDTLE
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                                                                                                                                                        Score 2518; DB 14;
Pred. No. 4.7e-209;
59; Mismatches 70;
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; SEQ ID NO 259
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo s
US-10-212-677-259
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APPLICANT: Xu, Jiangchun

APPLICANT: Fanger, Gary R.

APPLICANT: Harlocker, Susan L.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.484C7

CURRENT APPLICATION NUMBER: US/10/212,677

CURRENT FILING DATE: 2002-08-02

NUMBER OF SEQ ID NOS: 288

SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-212-677-259
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Matches 486
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                                                                                                                                                                      y Match 75.8%; Score 2518; DB 14; Local Similarity 75.8%; Pred. No. 4.7e-209; nes 486; Conservative 69; Mismatches 70;
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               FYGILPEIIGDCCYEEYKDRKRENAERLMDDNDSENNQES-MPSLSFRQTMWRAFENPHT 178
                                                       RYPDTLLGSSERDFFYHPETQQYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDEELA
                                                                    RYPDTLLGSTEKEFFFNEDTKEYFFDRDFEVFRCVLNFYRTGKLHYPRYECISAYDDELA 119
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GENERAL INFORMATION:

APPLICANT: Chenault, Ruth A.

APPLICANT: Chenault, Ruth A.

APPLICANT: Xu, Jiangchun

APPLICANT: Fanger, Gary R.

APPLICANT: Harlocker, Susan L.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.484C7

CURRENT APPLICATION NUMBER: US/10/212,677

CURRENT FILING DATE: 2002-08-02

NUMBER OF SEQ ID NOS: 288

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 260

LENGTH: 630

TYPE: PRT

ORGANISM: Homo sapiens
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US-10-212-677-260
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APPLICANT: Chenault, Ruth A.
APPLICANT: You, Jiangchun
APPLICANT: Fanger, Gary R.
APPLICANT: Harlocker, Susan L.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C7
CURRENT APPLICATION NUMBER: US/10/212,677
CURRENT APPLICATION NUMBER: US/10/212,677
CURRENT FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 288
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 261
LENGTH: 630
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US-10-212-677-261
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Publication No. US20030129192A1
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Best Local Similarity
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ORGANISM: Homo sapiens:-10-212-677-261
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                                                   FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPAS
                                                                                                                      HLLHCLEKTTNHEFIDEQMFEQNCMESSMQNYPSTRSPSLSSHPGLTTTCCSRRSKKTTH 537
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STLALVFYYVTGFFIAVSVITNVVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF
                                                                                                                                             RYPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELA 119
                                                                                                                                                                                               MAAGVAAWLPFARAAAIGWMPVASGPMPAPPRQERKRTQDALIVLNVSGTRFQTWQDTLE
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APPLICANT: FAIGER, GARY R.

APPLICANT: Fling, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CAN FILE REFERENCE: 210121.484C8

CURRENT APPLICATION NUMBER: US/10/361,811

CURRENT FILING DATE: 2003-02-05

NUMBER OF SEQ ID NOS: 293

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 258

LENGTH: 630

TYPE: PRT

ORGANISM: Homo sapiens

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Best Local Similarity
Matches 486; Conserv
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Pred. No. 4.7e-209;
59; Mismatches 70;
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Publication No. US20030206918A1

GENERAL INFORMATION:
APPLICANT: Fanger, Gary R.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THISTITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.484C8
CURRENT APPLICATION NUMBER: US/10/361,811
CURRENT FILING DATE: 2003-02-05
NUMBER OF SEQ ID NOS: 293
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 259
LENGTH: 630
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-811-259
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Sequence 260, Application US/10361811

Publication No. US20030206918A1

; GENERAL INFORMATION:
APPLICANT: Fanger, Gary R.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C8
CURRENT APPLICATION NUMBER: US/10/361,811
CURRENT FILING DATE: 2003-02-05
; MUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 260
; LENGTH: 630
TYPE: PRT
ORGANISM: Homo sapiens
US-10-361-811-260
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Fequence 261, Application US/10361811

Fublication No. US20030206918A1

GENERAL INFORMATION:

APPLICANT: Fanger, Gary R.

APPLICANT: Fling, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.484C8

CURRENT APPLICATION NUMBER: US/10/361,811

CURRENT FILING DATE: 2003-02-05

NUMBER OF SEQ ID NOS: 293

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 261

LENGTH: 630

TYPE: PRT

ORGANISM: Homo sapiens

US-10-361-811-261
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US-10-361-811-261
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KRRAQKKARLARIRVAKTGSSNAYLHSKRNGLLNEALELTGTPEEEHMGKTTSLIESQHH
                                                       FWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQNQRAD
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CURRENT APPLICATION NUMBER: US/10/369,186
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 293
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 258
LENGTH: 630
TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US20030232056A1
GENERAL INFORMATION:
APPLICANT: Fanger, Gary R.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS F
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN
FILE REFERENCE: 210121.484C9
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Pred. No. 4.7e-209;
69; Mismatches 70;
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; Publication No. US20030232056A1

; GENERAL INFORMATION:

; APPLICANT: Fanger, Gary R.

; APPLICANT: Fling, Steven P.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CAN

; FILE REFERENCE: 210121.484C9

; CURRENT APPLICATION NUMBER: US/10/369,186

; CURRENT FILING DATE: 2003-02-14

; NUMBER OF SEQ ID NOS: 293

; SOFTWARE: FastSEQ for Windows Version 4.0

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TYPE: PRT
ORGANISM: Homo s
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                                                                                             KRRAQKKARLARIRAAKSGSANAYMQSKRNGLLSNQLQ-SSEDEQAFVSKSGSSFETQHH
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APPLICANT: Fanger, Gary R.

APPLICANT: Fling, Steven P.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.484C9

CURRENT APPLICATION NUMBER: US/10/369,186

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 293

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 260

LENGTH: 630
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IPTPPALTPEGESRP--PPASPGPNTNIPSITSNVVKVSVL
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69; Mismatches 70;
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US-10-369-186-261
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APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C9
CURRENT APPLICATION NUMBER: US/10/369,186
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 293
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 261
LENGTH: 630
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## ALIGNMENTS

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R;Roberds, S.L.; Tamkun, M.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
A;Title: Cloning and tissue-specific expression of five voltage-gated potassium channel A;Reference number: A39113; MUID:91156694; PMID:1705709
A;Accession: A39113
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C;Keywords: channel-forming protein; ion channel; phosphoprotein; potassium channel
F;38/Binding site: phosphate (Thr) (covalent) (by cAMP- and cGMP-dependent kinases) #status
F;54,280,489,606/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status
F;70,447,531,537,548/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
F;101,166,291,316/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status
F;113,263,459,460,472,502,552/Binding site: phosphate (Ser) (covalent) (by casein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-476,'T','P',603-604,'ASL',608,'GENHE',614 <ROB>
A;Cross-references: GB:M59980; NID:g203467; PIDN:AAA40929.1; PID:g203468
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A;Title: Characterization of a mammalian cDNA for an inactivating A;Reference number: JU0271; MUID:92000693; PMID:1840649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 voltage-sensitive potassium channel protein [validated] - rat N;Alternate names: rat sha/1 C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004 C;Accession: JU0271; A39113
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A;Residues: 1-630 <BAL>
A;Residues: 1-630 <BI>
A;Cross-references: UNIPROT:Q63881; GB:S64320; NID:g236196; PIDN:AAB19939.1; PID:g236197
A;Experimental source: hippocampus
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                             RYPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELA 119
                                                                                                                                                                                                                                      MAAGVAAWLPFARAAAIGWMPVASGPMPAPPRQERKRTQDALIVLNVSGTRFQTWQDTLE
FFGLIPEIIGDCCYEEYKDRRRENAERLQDDADTDNTGESALPTMTARQRVWRAFENPHT
                                                                                                                      RYPDTLLGSSERDFFYHPETQQYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDEELA
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650 635 591 588 534 529 475 473 419 414

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RESULT
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C; Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change C; Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change C; Date: 20-Mar-1992 #sequence_revision A; Butler, A.; Ratcliffe, R; Pak, M.D.; Baker, K.; Covarrubias, M.; Butler, A.; Ratcliffe, Proc. Natl. Acad. Sci. U.S.A. 88, 4386-4390, 1991
A; Title: mShal, a subfamily of A-type K(+) channel cloned from m A; Reference number: A39372; MUID:91239573; PMID:2034678
A; Accession: A39372
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A;Molecule type: mRNA
A;Residues: 1-651 <PAK>
A;Cross-references: UNIPROT:Q03719; GB:M64226; NID:g199812; PIDN:AAA39745.1; PID:g199813
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C;Species: Drosophila melanogaster
C;Date: 14-Sep-1990 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C;Accession: A35312; S12747
R;Wei, A.; Covarrubias, M.; Butler, A.; Baker, K.; Pak, M.; Salkoff, L.
Science 248, 599-603, 1990
A;Title: K+ current diversity is produced by an extended gene family conservA;Reference number: A35312; MUID:90239553; PMID:2333511
A;Accession: A35312
                                                                                                                                                                                                                                                         A;Cross-references: EMBL:M32660; NID:g158456; PID:g158457
C;Genetics:
A;Gene: shal2
A;Cross-references: FlyBase:FBgn0005564
C;Superfamily: potassium channel protein drk1
C;Keywords: alternative splicing; ion channel; potassium of
                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P17971; GB:M32660; NID:g158456; PI R;Butler, A.; Wei, A.; Salkoff, L. Nucleic Acids Res. 18, 2173-2174, 1990
A;Title: Shal, Shab, and Shaw: three genes encoding potassium A;Reference number: S12746; MUID:90245668; PMID:2336395
A;Accession: S12747
A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-490 <BUT>
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 FGIMPDVIGDCCYEDYRDRKRENAERLMDDKLSENGDQNLQQLINMRQKMWRAFENPHTS
                YGILPEIIGDCCYEEYKDRKRENAERLMDDNDSENNQESMPSL-SFRQTMWRAFENPHTS
                                                                                                                              ASVAAWLPFARAAAIGWVPIATHPLPPPPMPKDRRKTDDEKLLINVSGRRFETWRNTLEK
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                                                                                                                                                                                         57.7%; Score 1915.5; DB 2; 73.6%; Pred. No. 1.4e-139; tive 61; Mismatches 63;
                                                                                                                                                                                                                                                          potassium channel; transmembrane
                                                                                                                                                                                             Indels
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120

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RESULT 5
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JH0595
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 20-C;Accession: JH0595
R;Hwang, P.M.; Glatt, C.E.; Bredt, D.S.; Yellen, G.; Snyder, S.H.
Neuron 8, 473-481, 1992
A;Title: A novel K+ channel with unique localizations in mammalian
A;Reference number: JH0595; MUID:92198655; PMID:1550672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: I57681

R; Rudy, B.; Kentros, C.; Vega-Saenz de Miera, E.C.

Rol. Cell. Neurosci. 2, 89-102, 1991

A; Title: Families of potassium channel genes in mai

A; Reference number: I57681

A; Accession: I57681
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-
C;Accession: I57681
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93.2%;
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; Pred. No. 1.9e.
2; Mismatches
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drk1
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A;Experimental source: circumvallate papillae
C;Superfamily: potassium channel protein drkl
C;Keywords: glycoprotein; phosphoprotein; transmembrane protein
F;191-212/Domain: transmembrane #status predicted <TM1>
F;233-254/Domain: transmembrane #status predicted <TM2>
F;265-286/Domain: transmembrane #status predicted <TM3>
F;299-320/Domain: transmembrane #status predicted <TM4>
F;335-356/Domain: transmembrane #status predicted <TM5>
F;339-418/Domain: transmembrane #status predicted <TM5>
F;337-418/Domain: transmembrane #status predicted <TM6>
F;347,287,419,446/Binding site: carbohydrate (Asn) #status
F;347,419,446/Binding site: carbohydrate (Asn) #status
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A; Residues: 1-802 < HWA>
A; Cross references: GB: M77482; NID: G203395;
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LLRFLSSPNKWKFFKGPLNVIDLLAILPYYVTIFLTESNKSVLQFQNVRRVVQIFRIMRI
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                                      PNCKTSQITTAIISIPTP-PALTPEGESRPPPASPGPNTNIPSITSNVVK 632
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Pred. No. 4.6e-51;
6; Mismatches 256
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R;Albrecht, B.; Lorra, C.; Stocker, K.; Pongs, submitted to the EMBL Data Library, September A;Description: Cloning, expression and chromos A;Reference number: S31761
A;Accession: S31761
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q14721; EMBL:X6830 C;Genetics:
A;Gene: GDB:KCNB1; KV2.1; DRK1
A;Gene: GDB:KCNB1; KV2.1; DRK1
A;Cross-references: GDB:128081; OMIM:600397
A;Map position: 20q13.2-20q13.2
C;Superfamily: potassium channel protein drk1
                                                                                                       RESULT
S00480
potassium channel protein A (clone Sh-beta) - fruit fly (Drosophila melanoga
C;Species: Drosophila melanogaster
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 17-Nov-2000
C;Accession: S00480; S01111
R;Pongs, O.; Kecskemethy, N.; Mueller, R.; Krah-Jentgens, I.; Baumann, A.; I
EMBO J. 7, 1087-1096, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C;Accession: S31761
R;Albrecht, B.; Lorra, C.; Stocker, K.; Pongs, O.
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expression and chromosomal
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Pred. No. 1.7e-49;
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                     H.H.;
RESULT 8
CHRTD1
potassium
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A;Title: Shaker encodes a family of putative potassium channel protein A;Reference number: S00479; MUID:88296413; PMID:2456921
A;Accession: S00480
A;Accession: S00480
A;Molecule type: DNA
A;Residues: 1-643 <PON>
A;Cross-references: EMBL:X07132; NID:g8602; PIDN:CAA30144.1; PID:g8603
A;Note: the clone is designated as Sh-beta
A;Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: S01113
A;Contents: annotation; erratum
C;Genetics:
A;Gene: Shaker
A;Cross-references: FlyBase:FBgn0003380
C;Superfamily: potassium channel protein drk1
C;Keywords: alternative splicing; transmembran
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A;Note: the clone is designated R;Schwarz, T.L.; Tempel, B.L.; F. Nature 332, 740, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Multiple potassium-channel components are produced A;Reference number: S00508; MUID:88122563; PMID:2448635 A;Accession: S01111 A;McCeule type: mRNA A;McCeule type: mRNA
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Nature 331, 137-142, 1988
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81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   AIMPYYIGLV----
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QTQQQLQQQQSHTINASAAAATSGSGSSGLT
                                ESSMQ-----
                                                                AVAPFLGAQQQQQPVASSLSMSIDKQLQHPLQQLTQTQLYQQQQQQQQQQQQQQQGFKQQQQ
                                                                                                                                                                  KARLARIRVAKTGSSNAYL-----HSKRNGL------LNEALELTGTPEEEHMGKT
                                                                                                                                                                                                   TMTTVGYGDMTPVGVWGKIVGSLCAIAGVLTIALPVPVIVSNFNYFYHRETDQEEMQSQN
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                                                                                                 ----TSLIESQHHHLLHCLEKTTNHEFIDEQM-----
                                                                                                                                 -TSCPYLPGTLGQHMKKSSLSESSSDMMDLDDGVESTPGLTETHPGRS
                                NYPSTRSPSLSSHPGLT
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Pred. No. 1.3e-48;
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A;Residues: 'MPAG',1-571 <DRE>
A;Cross-references: GB:M81783; NID:g205038
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P15387; EMBL:X16476; NID:g57785; PIDN:CAA34497.1; A;Note: it is uncertain whether Met-1 or Met-17 is the initiator R;Drewe, J.A.; Verma, S.; Frech, G.; Joho, R.H.

J. Neurosci. 12, 538-548, 1992

A;Title: Distinct spatial and temporal expression patterns of K+ channel mRNAs A;Reference number: A44838; MUID:92156897; PMID:1740690
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A; Residues: 1-853 < FRE>
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                                                                                                                                                                                 RFLSSPKKWKFFKGPLNAIDLLAILPYYVTIFLTESNKSVLQFQNVRRVVQIFRIMRILR
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                                                                                                                         ILKLARHSTGLQSLGFTLRRSYNELGLLILFLAMGIMIFSSLVFFÅEKDEDDTKFKSIPA
                                                                                                                                         IFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPA
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Pred. No. 1.9e.
30; Mismatches
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AKRNGSIVSMNMKDAFARSIEMMDIVVEKNGES
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A; Molecule type: DNA
A; Residues: 1-15 < RES>
A; Cross-references: GB:L23434; NID:g443766;
A; Experimental source: Sprague-Dawley
C; Genetics:
                                                                                                                                    C; Keywords: glycoprotein; phosphoprotein; potassium channel; F;242-260/Domain: transmembrane #status predicted <TM1> F;316-336/Domain: transmembrane #status predicted <TM2> F;317-368/Domain: transmembrane #status predicted <TM3> F;387-408/Domain: transmembrane #status predicted <TM4> F;423-444/Domain: transmembrane #status predicted <TM5> F;423-444/Domain: transmembrane #status predicted <TM6> F;484-505/Domain: transm
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R;Mori, Y.; Matsubara, H.; Folco, E.; Siegel, A.; Koren, J. Biol. Chem. 268, 26482-26493, 1993
A;Title: The transcription of a mammalian voltage-gated parameter number: I55392; MUID:94075338; PMID:8253777
A;Accession: I55392
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Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
A;Title: Cloning and tissue-specific expression of five A;Reference number: A39113; MUID:91156694; PMID:1705709
A;Accession: D39113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: KV1.5
C; Superfamily
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A;Title: Cloning and expression of cDNA and genomic clones
A:Reference number: JH0166; MUID:90297965; PMID:2361015
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C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change (C;Accession: JH0166; D39113; T55392
C;Accession: JH0166; D39113; T55392
C;Accession: JH0166; D39113; T55392
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A; Residues: 1-602 < SWA>
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N;Alternate names: potassium chann
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                                      Local Similarity
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                                22.2%;
Score 736; DB 2; 1
Pred. No. 1.3e-48;
0; Mismatches 162;
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(covalent) #status predicted
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APADKNKRQDELIVLNVSGRRFQTWRTTLERYPDTLLGSTEKEF-FFNEDTKEYFFDRDP 88

Matches

177;

Conservative

**90**;

Indels

Gaps

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A;Nolecule type: mRNA
A;Residues: 1-512,514-564,'Q',565-583,'HV',586-656 <SCH>
A;Residues: GB:X06742; NID:g288441; PIDN:CAA29917.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-656 < KAM>
A; Residues: 1-656 < KAM>
A; Residues: 1-656 < KAM>
A; Cross-references: UNIPROT: P08510
A; Cross-references: UNIPROT: P08510
A; Note: the sequence Tyr-Phe-Ile-Thr, residues 323-326, is present in the p R; Schwarz, T.L.; Tempel, B.L.; Papazian, D.M.; Jan, Y.N.; Jan, L.Y.
Nature 331, 137-142, 1989
A; Title: Multiple potassium-channel components are produced by alternative A; Reference number: S00508; MUID: 88122563; PMID: 2448635
A; Accession: S00508
A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       potassium channel shaker form epsilon - fruit fly (Drosophila melanogaster) N;Alternate names: potassium channel protein A C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text change 09-Jul-2004 C;Accession: JH0193; S00508; S01110; S00479; S00482; S02822; S01674 R;Kamb, A.; Tseng-Crank, J.; Tanouye, M.A. Neuron 1, 421-430, 1988 A;Title: Multiple products of the Drosophila Shaker gene may contribute to 1 A;Reference number: JH0193; MUID:90166523; PMID:3272175 A;Accession: JH0193
                                                                                                      A; Molecule type: DNA
A; Residues: 'MQMI',57,'VAG',61-452,'F',454-462,'VV',465-488,'A',490,'R',492-505,'S',507-
A; Residues: 'MQMI',57,'VAG',61-452,'F',454-462,'VV',465-488,'A',490,'R',492-505,'S',507-
,'QL',577-579,'LQ',582-584,'QS',587,'SPHG',592-593,'MT',596-599,'LG',602-604,'LRS','TNS'
R; Pongs, O.; Kecskemethy, N.; Mueller, R.; Krah-Jentgens, I.; Baumann, A.; Kiltz, H.H.;
EMBO J. 7, 1087-1096, 1988
A; Title: Shaker encodes a family of putative potassium channel proteins in the nervous same proteins of the nervous same proteins in the nervous same proteins of the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins in the nervous same proteins 
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A; Molecule type: DNA
A; Residues: 1-452, 'F', 454-462,'V', 464-488, 'A', 490, 'R', 492-505, 'S', 507-510, 'A', 512, 514-51
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                                                                             A; Accession: S00479
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A;Introns: 61/2; 102/3; 159/1; 191/2; 256/3; 297/2; 348/3; 406/1; C;Superfamily: potassium channel protein drk1
C;Keywords: alternative splicing; glycoprotein; phosphoprotein; po F;228-246/Domain: transmembrane #status predicted <TM1>F;279-300/Domain: transmembrane #status predicted <TM2>F;311-332/Domain: transmembrane #status predicted <TM3>F;358-382/Domain: S4-like region #status predicted <TM4>F;358-382/Domain: transmembrane #status predicted <TM4>F;432-453/Domain: transmembrane #status predicted <TM5>F;457-478/Domain: transmembrane #status predicted <TM6>F;457-478/Domain: transmembrane #status predicted <
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A;Accession: S02822

A;Molecule type: mRNA
A;Residues: 1-452,'F',454-462,'VV',465-488,'A',490,'R',492-505,'S',507-510,'A',512,514-51
A;Residues: 1-452,'F',454-462,'VV',465-488,'A',490,'R',492-604,'LRS','TNS',640,'QL',643-647,
A;Residues: 1-452,'F',454-462,'VV',465-488,'A',490,'R',492-505,'S',507-510,'A',512,514-51
A;Residues: 1-452,'F',454-462,'VV',465-488,'A',490,'R',492-505,'S',507-510,'A',512,514-51
A;References: EMBL:X07131; NID:g8600; PID:g8601
R;Tempel, B.L.; Papazian, D.M.; Schwarz, T.L.; Jan, Y.N.; Jan, L.Y.
Science 237, 770-775, 1987
A;Reference number: S01674; MUID:87292096; PMID:2441471
A;Accession: S01674; MUID:87292096; PMID:2441471
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A;Accession: S00482
A;Molecule type: DNA
A;Residues: 1-348,'V' <PO2>
A;Cross-references: EMBL:X07134; NID:g8606; PIDN:CAA30146.1; PID:g8607
R;Pongs, O.
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A; Molecule type: mRNA
A; Residues: 1-452, 'F', 454-462, 'VV', 465-488, 'A', 490, 'R', 492-505, 'S', 507-510, 'A', 512,514-51
', 582-584, 'QS', 587, 'SPHG', 592-593, 'MT', 596-599, 'LG', 602-604, 'LRS', 'TNS', 640, 'QL', 643-647,
A; Cross-references: EMBL:M17211; NID:g157063; PIDN:AAA28417.1; PID:g157064
A; Note: 360-Met and 464-11e were also found
C; Comment: This protein is a component of a fast, transient, voltage-dependent, or A-type C; Genetics:
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A;Cross-references:
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      TMTTVGYGDMTPVGVWGKI VGSLCAI AGVLTI ALPVPVI VSNFNYFYHRETDQEEMQSQN
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RESULT 11
S12746
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C;Species: Drosophila melanogaster
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S12746; S15058
R;Butler, A.; Wei, A.; Salkoff, L.
Nucleic Acids Res. 18, 2173-2174, 1990
A;Title: Shal, Shab, and Shaw: three genes encoding potassium channels in D; A;Reference number: S12746; MUID:90245668; PMID:2336395
A;Accession: S12746
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C;Superfamily: potassium channel protein drk1
C;Keywords: ion channel; potassium channel; transmembrane protein
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A; Residues: 1-924 < BUT>
A; Cross-references: UNIPROT: P17970; EMBL: M32659
R; Butler, A: Wei, A: Salkoff, L.
submitted to the EMBL Data Library, March 1990
A; Description: Shal, Shab, and Shaw: Three gene.
A; Reference number: S15058
A; Accession: S15058
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A;Residues: 1-625,'YG',628-924 <BU2>
A;Cross-references: EMBL:M32659; NID:g158458;
C;Genetics:
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A;Title: A mouse brain homolog of the Drosophila Shab K+
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C;Superfamil
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C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
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A; Residues: 1-857 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: I56529
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PID:g200976

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RESULT 14
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potassium
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R;Sasaki, Y.; Ishii, K.; Nunoki, K.; Yamagishi, T.; Taira, FEBS Lett. 372, 20-24, 1995
A;Title: The voltage-dependent K(+) channel (Kv1.5).cloned A;Reference number: S66669; MUID:96032538; PMID:7556635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   potassium channel (Kv1.5) - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change
C;Accession: S66669
R;Sasaki, Y.; Ishii, K.; Nunoki, K.; Yamagishi, T.; Taira, N.
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A; Residues: 1-598 < SAS>
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                                                                                                   NQRADKRRA----
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                                                                                                                                                                                                                                                                       APSRYRFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGA------FVTLRVF
                                                                                                                                                                                                                                                                                                                                                                                     MPSLSFRQTMWRAFENPHTSTLALVFYYVTGFFIAVSVITNVVETVP-------
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                                                                       ETDHEEQAALKEEPGSQSRGTSLDAGGQRKASWSKASLCKAGGSLETADSVRRG
                                                                                                                                SIPDAFWWAVVTMTTVGYGDMRPITVGGKIVGSLCAIAGVLTIALPVPVIVSNFNYFYHR
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                                                                                                                                                                                                                                                                                                                   -GKLHYPRYECISAYDDELAFYGILPEIIGDCCYEEYKDRKRENAERLMDDNDSENNQES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
   Kv1.5
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35.0%; Pre
ative 85;
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Pred. No. 2.6e-
85; Mismatches
                                                                                                   OKKARLARIRVAKTGSSNAYLHSKRNG 448
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C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-0
C;Accession: A49507; B49507
R;Attali, B.; Lesage, F.; Ziliani, P.; Guillemare, E.; Honore, E.; I
J. Biol. Chem. 268, 24283-24289, 1993
A;Title: Multiple mRNA isoforms encoding the mouse cardiac Kv1-5 del
A;Reference number: A49507; MUID:94043264; PMID:8226976
A;Accession: A49507
A;Molecule type: mRNA
A;Residues: 1-602 <ATT>
A;Cross-references: UNIPROT:Q61762; GB:L22218; NID:g435603; PIDN:AAJ
A;Accession: B49507
A;Status: preliminary
A;Accession: B49507
A;Status: preliminary
A;Accession: B49507
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 201-602 <AT2>
A; Cross-references: GB:L22218
C; Superfamily: potassium channel protein
C; Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSFDGILYYYQSGGRLRRPVNVSLDVFADEIRFYQ-----LGDEAMERFRE-----
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                                                                                                                                                                                                                                                                SLAILRVIRLVRVFRIFKLSRHSKGLQILGKTLQASMRELGLLIFFLFIGVILFSSAVYF
                                                                                                                                                                             IMPTFELLVRFFACPSKAEFSRNIMNIIDIVAIFPYFITLGTELAEQQFGGGGQQQAM
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DSIRRGSCPLEKCHLKAKSNVDLRRSLYALCLD
                                        EALELTGTPEEEHMGKTTSLIESQHHHLLHCLE
                                                                                       IVSNFNYFYHRETDHEEQAALKEEQGIQRRESGLDTGGQRKVSCSKASFH-KTGGPLEST
                                                                                                                                IVSNFSRIYHQNQRADKRRAQKKARLARIRVA-----KTGSSNAYLHSKRNGLL--N
                                                                                                                                                                                                  AEKGSSASKFTSIPASFWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPV
                                                                                                                                                                                                                                                                                      ----FVTLRVFRVFRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFY
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Pred. No. 2.6e-47;
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potassium channel KV1.3 - rat
N;Alternate names: potassium channel Kv3; potassium channel R
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1992 #sequence revision 28-Oct-1992 #text\_chan
C;Accession: A43531; JH0168; S06708
R;Douglass, J.; Osborne, P.B.; Cai, Y.C.; Wilkinson, M.; Chri
J. Immunol. 144, 4841-4850, 1990
A;Title: Characterization and functional expression of a rat of A;Reference number: A43531; MUID:90278098; PMID:2351830 M.; Christie, \_change RCKG; genomic DNA clone encoding 09-Jul-2004 potassium M.J.; Adelman, channel RGK5

RLARIRVAKTGSSNAYLHSKRN 447  : YMH 451	oo in oo be	Db 415
4 4 4	) D	41
	8 SLSGVLVIALÞVÞVIVSNFSRIYHQNQRADKRRAQKKARLARIRVAKTGSSNAYLHSKRN	Qy 388
IPASFWYTIVTMTTLGYGDMVPKTIAGKIFGSIC 387	и — н	3 3 5 8
TLRVFRVFRIFKFSRHSQGLRILGYTLKSCASELGFLLFS 327	6 MTINEDVSGAFV- ; ;     ; 5 TELAERQGNGQQAMSLAILH	9 7
FIRSYMSIIDVVAIMPYYIGLV 275	9GERYSVAFFCLDTACVMIFTVEYLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLV :\	Qy 219 Db 235
TVPGSKELPC218	6 PHTSTLALVFYYVTGFFIAVSVITNVVETVPCG   :	Qy 176 Db 177
DDNDSENNQESMPSLSFRQTMWRAFEN 175  : :    :::     DEGFLREEERPLPRRDFQRQVWLLFEY 176	6 DELAFYGILPEIIGDCCYEEYKDRKRENAERLM 	Qy 116 Db 132
EVFRCVLNFYRT-GKLHYPRYECISAYD 115	8 LERYPOTILGSTEKEF-FFNEDTKEYFFDRDF   :: :     :: : :       : 2 LCQFPETLLGDPKRRMRYFDPLRNEYFFDRNR	Qy 58 Db . 72
KRQDELIVLNVSGRRFQTWRTT 57 	O PFARAAAIGMMPVANCPMPLAPADKNKRQDELIVLNVSGRRFQTWRT	Qy 10 Db 12
; Length 525; ; Indels 113; Gaps 16;	h 21.6%; Score 718.5; DB 2 Similarity 31.0%; Pred. No. 2.4e-47; 78; Conservative 104; Mismatches 179	Query Match Best Local Matches 17
s, J.B.; Boyle, M.B.; Folander, K.; Lunic clones encoding three delayed rectif 361015  AAA41500.1; PID:g205105  S06708 is given .; Sakmann, B.; Stocker, M.; Giese, K.F. of voltage-gated potassium channels in 555158  :CAA34132.1; PID:g57035  um channel; tetramer; transmembrane pro <tm1> <tm2> <tm4> <tm4> <tm4> <tm5> <tm5> us predicted <tmb1> us predicted <tmb1> us predicted <tmb2> <tm6> <tm6> <tm6>  CAMP-dependent kinase) #status predicted <tmb2></tmb2></tm6></tm6></tm6></tmb2></tmb1></tmb1></tm5></tm5></tm4></tm4></tm4></tm2></tm1>	PROT: P15384; GB:M30312 1, J.; Smith, J.S.; William 0 0166; MUID: 90297965; PMID: 2 182-525 <swa> :M31744; NID: 90297965; PMID: 2 brain differences from sequence sberg, J.P.; Schroeter, K.H 1989 is of functional diversity 6708; MUID: 90059914; PMID: 2 6708; MUID: 90059914; PMID: 2 brain in; phosphoprotein; potassismembrane #status predicted smembrane beta strand #status predicted smembrane beta strand #status predicted smembrane beta strand #status predicted smembrane beta strand #status predicted smembrane beta strand #status predicted smembrane #status p</swa>	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-525 < DOU A;Cross-references: UN R;Swanson, R.; Marshal Neuron 4, 929-939, 199 A;Title: Cloning and e A;Reference number: JH A;Accession: JH0168 A;Molecule type: DNA A;Residues: 1-180, 'G', A;Cross-references: GB A;Kote: only a list of R;Stuehmer, W.; Rupper EMBO J. 8, 3235-3244, A;Title: Molecular bas A;Reference number: S0 A;Accession: S06708 A;References: EMBO J. 8, 3235-3244, A;Title: Molecular bas A;Reference number: S0 A;Accession: S06708 A;Cross-references: EMBO A;Accession: S06708 A;Cross-references: EMC;Keywords: glycoprote F;185-203/Domain: tran F;245-266/Domain: tran F;248-367/Domain: tran F;313-331/Domain: tran F;383-392/Domain: tran F;383-392/Domain: tran F;383-392/Domain: tran F;393-401/Domain: tran F;393-401/Domain: tran F;470/Binding site: ph

Search completed: April 6, 2005, 07:17:45 Job time : 116.785 secs This Page Blank (uspto)

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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  Score
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seq length: 2000000000
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Match
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3320
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1: uniprot_sprot:*
2: uniprot_trembl:*
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  MAAGVAAWLPFARAAAIGWM......PGPNTNIPSITSNVVKVSVL
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Q9PTD3
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O57662 xenopus lae
Q7zw36 brachydanio
Q8hyz1 mustela put
P59995 oryctolagus
Q9z0v2 mus musculu
Q63881 rattus norv
Q9nzv3 norv
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Q62897 rattus norv
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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32
750	750.5	754.5	. 756	758	766	766	767.5	768	770	837	1103	1328.5	1654.5
22.6	22.6	22.7	22.8	22.8	23.1	23.1	23.1	23.1	23.2	25.2	33.2	40.0	49.8
858	876	816	911	985	911	898	908	911	907	409	236	478	372
_	N	N	ب	<b>-</b>	۲	N	Ŋ	N	r	N	N	N	N
KCB1_HUMAN	Q91593	Q98SV4	KCB2_RABIT	CIKB_DROME	KCB2_HUMAN	Q91592	018476	Q7Z7D0	KCB2_RAT	P91783	Q619B6	P91784	Q75LS7
Q14721 homo sapien	Q91593 xenopus lae		Q95111 oryctolagus			Q91592 xenopus lae						P91784 polyorchis	Q751s7 homo sapien

## ALIGNMENTS

REPORT RE	22	R R R R R R R R R R R R R R R R R R R	RESUI RESUI PAC AC DI DI DI DI DI DI DI DI DI DI DI DI DI
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.  TISSUE=Brain cortex;  MEDLINE=20195625; PubMed=10729221; DOI=10.1006/geno.2000.6117;  Isbrandt D., Leicher T., Waldschuetz R., Zhu XR., Luhmann U.,  Michel U., Sauter K., Pongs O.;  "Gene structures and expression profiles of three human KCND (Kv4)  potassium channels mediating A-type currents I(TO) and I(SA).";  Genomics 64:144-154(2000).  [5]  INTERACTION WITH KCNIP2; KCNE1; KCNE2; SCN1B AND KCNAB1.  MEDLINE=22233757; PubMed=12297301; DOI=10.1016/S0014-5793(02)03296-9;  Deschenes I., Tomaselli G.F.;  "Modulation of Kv4.3 current by accessory subunits.";	MEDLINE=99218223; PubMed=10200233; Dilks D., Ling HP., Cockett M., Sokol P., Numann R.; Pilks D., Ling HP., Cockett M., Sokol P., Numann R.; Pilks D., Ling HP., Cockett M., Sokol P., Numann R.; Pilks D., Ling HP., Cockett M., Sokol P., Numann R.; Pilks D., Ling HP., Cockett M., Sokol P., Numann R.; Pilks D., Rouanel."; Pilks T. P. G., Faivre JF., Javre JL., Cheval B., Rouanet S., Pril A.; Pilks D., Rouanet S., Davre JL., Cheval B., Rouanet S., Pril A.; Plant B., Rouanet S., Pril A.; Plant B., Rouanet S., Pril A.; Plant B., Rouanet S., Pril A.; Plant B., Rouanet S., Pril A.; Plant B., Rouanet S., Pril A.; Plant B., Rouanet S., Pril A.; Plant B., Rouanet S., Pril A.; Plant B., Rouanet S., Pril A.; Plant B., Rouanet S., Pril A.; Plant B., Rouanet S., Pril A.; Plant B., Rouanet S., Pril A.; Pril A.; Plant B., Rouanet S., Pril A.; Pril	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), TISSUE SPECIFICITY, AND FUNCTION.  TISSUE-Heart;  MEDLINE-99061682; PubMed=9843794;  MEDLINE-99061682; PubMed=9843794;  Kong W., Po S., Yamagishi T., Ashen M.D., Stetten G., Tomaselli G.F.;  "Isolation and characterization of the human gene encoding Ito:  "Isolation and characterizative mRNA splicing.";  further diversity by alternative mRNA splicing.";  Am. J. Physiol. 275:H1963-H1970(1998).  [2]  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND TISSUE SPECIFICITY.  TISSUE-Brain, and Heart;	RESULT 1  KCD3_HUMAN STANDARD; PRT; 655 AA.  ID KCD3_HUMAN STANDARD; PRT; 655 AA.  AC Q9UK17; O60576; O60577; Q9UH85; Q9UH86; Q9UK16;  AC Q9UK17; O60576 (Rel. 43, Created)  DT 29-MAR-2004 (Rel. 43, Last sequence update)  DT 05-JUL-2004 (Rel. 44, Last annotation update)  DF Potassium voltage-gated channel subfamily D member 3 (Voltage-gated potassium voltage-gated channel subfamily D member 3 (Voltage-gated DE potassium channel subunit Kv4.3).  GN Name=KCND3;  OS Homo sapiens (Human).  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  OX NCBI_TaxID=9606;

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Genew; HGNC:6237, ....

R MIM; 605411; -...

R InterPro; IPR005821; Ion_trans.

R InterPro; IPR001622; K+channel_pore.

R InterPro; IPR003091; K channel.

R InterPro; IPR003131; K_tetra.

DR InterPro; IPR004056; KV43channel.

DR InterPro; IPR003968; Kv_channel.

DR InterPro; IPR003968; Kv_channel.

DR InterPro; IPR003975; Shal_channel.

InterPro; IPR003975; Shal_channel.
    Pfam; PF00520; Ion trans; 1.
Pfam; PF02214; K tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01518; KV43CHANNEL
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01497; SHALCHANNEL
Alternative splicing; Ion tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF120491; AAD38898.1; -
EMBL; AF166011; AAF68177.1; -
EMBL; AF166009; AAF68177.1; J
EMBL; AF166010; AAF68177.1; J
EMBL; AF166010; AAF68178.1; -
EMBL; AF166010; AAF68178.1; J
EMBL; AF166010; AAF68178.1; J
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EMBL; AF166010; AAF68178.1; J
EMBL; AF166010; AAF68178.1; J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=KCND3L, Long;
IsoId=Q9UK17-1; Sequence=Displayed;
Name=2; Synonyms=KCND3S, Short;
IsoId=Q9UK17-2; Sequence=VSP_008826;
TISSUE SPECIFICITY: Highly expressed in heart and brain, in particular in cortex, cerebellum, amygdala and caudate nucleus.
Detected at lower levels in liver, skeletal muscle, kidney and pancreas. Isoform 1 predominates in most tissues. Isoform 1 and isoform 2 are detected at similar levels in brain, skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial itles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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DOMAIN: The segment S4 is probably the voltage-sensor a characterized by a series of positively charged amino a every third position.

SIMILARITY: Belongs to the potassium channel family. D
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SUBUNIT: Homotetramer or heterotetramer with KCND1 and/or KCND2.
SUBUNIT: Homotetramer or heterotetramer with KCND1 and/or KCND2.
KCNIP4 (By similarity). Interacts with KCNE1, KCNE2, SCN1B and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; AF048712; AAC05121.1; -.; AF048713; AAC05122.1; -.; AF187963; AAF01044.1; -.; AF187964; AAF01045.1; -.; AF205856; AAF20924.1; -.; AF205857; AAF20925.1; -.; AF205491; AAD388981; -.; AF206491; AAD388981; -.; AF206491; AAD388981; -.; AF206491; AAD388981; -.; AF266177.1; 
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01491; KVCHANNEL.
01497; SHALCHANNEL.
e splicing; Ion transport; Ion
Potassium channel; Potassium
                                                                        Voltage-gated
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Cytoplasmic (Segment S1 (F) Segment S2 (F)
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  (Potential).
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(Potential).
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            LRPNCKTSQITTAIISIPTPPALTPEGESRPPPPASPGPNTNIPSITSNVVKVSVL
                                      GLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDG
                                                 GLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDG
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Segment S3 (Potential).
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Pred. No. 7.7e-198;
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P -> L (in Ref. 1).
R -> G (in Ref. 2).
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T -> Q (in Ref. 2).
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A -> T (in Ref. 1).
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filter (By similarity).
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RESULT 2
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MEDLINE=22128857; Pubm
Takimoto K., Yang P.
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An W.F., Bowlby M.
Hinson J.W., Matt
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MEDLINE=97460452; PubMed=9314834;
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STRAIN=Sprague-Dawley; TISSUE=Uterus;
MEDLINE=21402960; PubMed=11427525; DOI=10.
Song M., Helguera G., Eghbali M., Zhu N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION TISSUE=Smooth muscle, and Vas deferens; MEDLINE=98111009; PubMed=9450548; DOI=100 Chya S., Tanaka M., Oku T., Asai Y., Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 2), F
MEDLINE=96428386; PubMed=8831489;
Dixon J.E., Shi W., Wang H.-S., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potassium voltage-gated chepotassium channel subunit Name=Kcnd3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-2004 (Rel. 43, Createu,
29-MAR-2004 (Rel. 43, Last sequence update)
29-MAR-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning and tissue variant of an A-type K+ chann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serodio P., Vega-Saenz de Miera E., Rudy B.; "Cloning of a novel component of A-type K+ channels subthreshold potentials with unique expression in he J. Neurophysiol. 75:2174-2179(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     correlate for the transient outward Circ. Res. 79:659-668(1996).
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Cohen I.S., McKinnon D.;
                                                                                                                                                                                                             INTERACTION WITH KCNIP1; KCNIP2 ANI
MEDLINE=20140134; PubMed=10676964;
                                                                                                                                                                                                                                                                          Takimoto K., Li D., Hershman K.M., Li P., Jackson E.K., Le "Decreased expression of Kv4.2 and novel Kv4.3 K+ channel mRNAs in ventricles of renovascular hypertensive rats."; Circ. Res. 81:533-539(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Foro L., Stefar "Remodeling of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97154683; P
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Lett. 420:47-53(1997)
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                                                                                                                                            Bowlby M.R., Betty M., Cao J., Ling .W., Mattsson K.I., Strassle B.W., T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stefani E.;
ing of Kv4.3 potassium channel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7154683; PubMed=9001401; DOI=10.:
L., Chou C.-C., Shih Y.-H., Wang expression and CNS distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      400:215-220(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                              hormones.";
276:31883-31890(2001).
                    PubMed=12006572; DOI=10.1074/jbc.M203651200; E.-K., Conforti L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=8734615
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Y., Watanabe M., Giles W.R.,
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                                                                                                                                              DOI=10.1038/35000592;
o J., Ling H.-P., Mendoza G.,
le B.W., Trimmer J.S., Rhodes
annels by a family of calcium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q62897-3; Sequence=VSP_008831, VSP_008832; TISSUE SPECIFICITY: Highly expressed in brain, in particular the retrosplenial cortex, medial habenula, anterior thalamus, hippocampus, cerebellum and lateral geniculate and superior colliculus. Highly expressed in heart atrium and throughout the ventricle wall, in lung and vas deferens.

DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
SUBCELLULAR LOCATION: Integral palmitoylated KCNIP2 and KCN ALTERNATIVE PRODUCTS:
Event=Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     every third position.
SIMILARITY: Belongs to the potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulatory subunits.
SUBUNIT: Homotetramer or heterotetramer with Associates with the regulatory subunits KCNIP KCNIP4. Interacts with KCNE1, KCNE2, SCNIB an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Pore-forming (alpha) subunit of voltage-gated inactivating A-type potassium channels. May contribute tourrent in heart and I(Sa) current in neurons. Channel pare modulated by interactions with other alpha subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=3
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IsoId=Q62897-1; Sequence=Displayed;
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3 enhances cell su
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InterPro; IPR005821; Ion trans.
InterPro; IPR001622; K+channel pore.
InterPro; IPR001622; K+channel pore.
InterPro; IPR003091; K\_channel.
InterPro; IPR003131; K\_tetra.
InterPro; IPR004056; KV43channel.
InterPro; IPR004056; KV43channel plg.
InterPro; IPR005820; M+channel plg.
InterPro; IPR005820; M+channel plg.
InterPro; IPR003975; Shal\_channel.
Pfam; PF00520; Ion\_trans; 1.
Pfam; PF00520; Ion\_trans; 1.
Pfam; PF00520; Ion\_trans; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01491; KVCHANNEL. EMBL; U42975; AAC52695.1; -. EMBL; U75448; AAB18337.1; -. EMBL; L48619; AAA80459.1; -. EMBL; AF334791; AAK07651.1; -. EMBL; AB003587; BAA24525.1; -. EMBL; U92897; AAB53321.1; -. HSSP; Q16968; 1A68. use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch). and is in collaboration -.ch/ n no way /announce/

Ion transport;

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601 LRPNCKTSQITTAIISIPTPPALTPEGESRPPPASPGPNTNIPSITSNVVKVSVL

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                                      GLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDG
                                                                                                                                                                                             SRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPASFWY
                                                                                                                                                                                                                                 YLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGAFVTLRVFRVFRIFKF
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                                                                                                                                                                                                                                                                                                                                                   YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF
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                                                                                       HCLEKTT
                                                                                                                    AQKKARLARIRVAKTGSSNAYLHSKRNGLLNEALELTGTPEEEHMGKTTSLIESQHHHLL
                                                                                                                                             TIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQNQRADKRR
                                                                                                                                                          TIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQNQRADKRR
                                                                                                                                                                                                                        YLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGAFVTLRVFRVFRIFKF
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                             GLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDG
                                                                   HCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMFEQNCMESSMQNYPSTRSPSLSSHS
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Segment H5
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Selectivity filter (By similarity)
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Segment S4 (Potential).
Cytoplasmic (Potential).
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-> QDQEQPRGRVVTCKQEEIITLCI (in
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DC __SYZOVII
CC __SYZOVII
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RC STRAIN=22354683; PNbMed=12466851; DOI=10.1038/nature01266;

RX MEDLINE=22354683; PNbMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldke J.A., Eradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

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RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kanajaya A., Kurochkin I V., Lee Y., Lenhard B., Lyons P.A.,

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RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Nagashima T., Nahita R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Yang I.,

RA Yasunishi A., Yanghaw-Boris A., Yangi Sawa M., Yang I., Yang I.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Hara A., Hashizume W., Imotani X., Ishii Y., Itoh M., Kagawa I.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Yasunishi A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Schonsele T., Konso Based on functional annotation of the mouse transcriptome based on functional annotation of
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MEDLINE=21906624; PubMed=11909823;

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Guo W., Li H., Aimond F., Johns D.C., R!
Guo W., Li M.;

"Role of heteromultimers in the generat outward K+ currents.";
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29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Potassium voltage-gated channel subfamily D m
potassium channel subunit Kv4.3).
                                                                                                                                                                                                                                                                                    INTERACTION WITH KCNIP3.

MEDLINE=21481767; PubMed=11598014; DOI=10.

Liss B., Franz O., Sewing S., Bruns R., Ne
"Tuning pacemaker frequency of individual

Kv4.3L and KChip3.1 transcription.";

EMBO J. 20:5715-5724(2001).
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Mammalia; Eutheria;
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InterPro; IPR003091; K_channel.
InterPro; IPR003131; K_tetra.
InterPro; IPR004056; KV43channel.
InterPro; IPR003968; Kv_channel.
InterPro; IPR003975; Shal_channel.
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Pfam; PF02214; K tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01491; KV43CHANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01497; SHALCHANNEL.
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                                                                                                                                                                                                                            Transport;
                                                                                                                TRANSMEM TRANSMEM
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   VARSPLIC
                                                                                                                                                                                                                                                         Alternative splicing; Ion transport; Ion Potassium Channel; Potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF107781; AAD16973.1;
EMBL; AF107782; AAD16974.1;
EMBL; AK033962; BAC28529.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  + +
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                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; Q16968; 1A68
MGD; MGI:1928743;
                                                                                     DOMAIN
                                                           VARSPLIC
                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     every third position. SIMILARITY: Belongs to the potassium channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=1; Synonyms=Kv4.3L;
IsoId=Q9Z0V1-1; Sequence=Displayed;
Name=2; Synonyms=Kv4.3M;
IsoId=Q9Z0V1-2; Sequence=VSP_008827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regulatory subunits.
SUBUNIT: Homotetramer or heterotetramer with KCND1 and/or KCND2.
Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly inactivating A-type potassium channels. May contribute to I(To) current in heart and I(Sa) current in neurons. Channel properties are modulated by interactions with other alpha subunits and with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subtamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KCNIP4. Interacts with KCNE1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q9Z0V1-3; Sequence=VSP_008828, Note=May be due to intron retention. confirmation available;
                                                                                                                                                                                                                                          Voltage-gated
   488
                                                          182
222
243
257
287
287
287
308
321
360
360
360
367
403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1A68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kcnd3
  506
                                                          181
202
242
256
277
277
307
320
341
341
402
5372
5372
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                                                                                                                                                                                                                                           channe.
                                                                                              Cytoplasmic (Potential).
Segment S1 (Potential).
Segment S2 (Potential).
Cytoplasmic (Potential).
Segment S3 (Potential).
Segment S4 (Potential).
Segment S4 (Potential).
Cytoplasmic (Potential).
Segment S5 (Potential).
Segment H5 (pore-forming)
Segment H5 (pore-forming)
                 Segment S6 (Potential).
Segment S6 (Potential).
Cytoplasmic (Potential).
Selectivity filter (By similarity).
Selectivity filter (By similarity).
GLSYLVDDPLLSVRTSTIKNHEFIDEQMFEQNCMESSMQNY
PST -> VSSSLLPPPASSLTSQGCTHVIIPRRESSSVPFQ
CVTTVSLPLG (in isoform 3).
SKTIVSLPLG (
/FTId=VSP_00
Missing (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KCNE2,
                                                                                                                                                                                                                                                                       Ionic channel; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        noved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
              008828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no restrictions ong as its content is in
                                                                                                (pore-forming) (Potential).
                                                                                                                                                                                                                                                         transport;
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  isoform
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No experimental
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                                                                                                               (Potential)
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RESULT 4

KCD3_RABIT

ID KCD3_RABIT

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Rae J.
                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Lagomorpha; Leporidae;
NCBI TaxID=9986;
                                                                                                                  29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Potassium voltage-gated channel subfamily D m
potassium channel subunit Kv4.3).
                        STRAIN=New
                                  SEQUENCE
                                                                                                          Name=KCND3;
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channels
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                      FROM N.A.
ew Zealand
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                                                                                                                                                                                                                                                                                                                         GLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDG
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                                                                                                                                                                                                                                                       LRPNCKTSQITTAIISIPTPPALTPEGESRPPPASPGPNTNIPS
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                                                                                                                                                                                                                                                                                                                                                                              HCLEKTT----
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in
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cornea
                       white;
                      (ISOFORM 1). white; TISSUE=Corneal
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endothelium.";
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Pred. No. 8.9
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Missing (in isoform 3).
/FTId=VSP_008829.
/ 17FCE5AEC2868B33 CRC64;
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                                                                    Vertebrata; Eu
ae; Oryctolagus
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es 3;
                       endothelium
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                                                                                                                              member 3 (Voltage-gated
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InterPro; IPR001622; K+channel pore.
InterPro; IPR003091; K_channel.
InterPro; IPR003131; K_tetra.
InterPro; IPR004056; KV43channel.
InterPro; IPR004056; KV channel.
InterPro; IPR003968; KV channel.
InterPro; IPR005820; M+channel_nlg.
InterPro; IPR005820; M+channel_nlg.
                                                                                                                                                                                                                                            InterPro; Irans; I.

Pfam; PF00520; Ion_trans; I.

Pfam; PF02214; K_tetra; 1.

Pfam; PF02214; K_tetra; 1.

PRINTS; PR010169; KCHANNEL.

PRINTS; PR01518; KV43CHANNEL.

PRINTS; PR01491; KVCHANNEL.

PRINTS; PR01497; SHALCHANNEL.

Alternative splicing; Ion transport; Ionic channel; Multigene family; Potassium; Potassium channel; Potassium transport; Transmembrane; Potassium; Potassium channel.

Propresent: Voltage-gated channel.
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EMBL; AF493549; AA
HSSP; Q16968; 1A68
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sanchez D., Lopez-Lopez J.R., Perez-Garcia M.T. Obeso A., Ganfornina M.D., Gonzalez C.; "Molecular identification of Kv alpha subunits
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IsoId=Q9TTT5-1; Sequence=Displayed;
Name=2; Synonyms=Short;
IsoId=Q9TTT5-2; Sequence=VSP_008830;
TISSUE SPECIFICITY: Detected in carotid body chemoreceptor cells and in frontal cortex.

DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
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SUBUNIT: Homotetramer or heterotetramer with KCND1 and/or KCND2.
Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 a
KCNIP4. Interacts with KCNB1, KCNB2, SCNIB and KCNAB1 (By
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FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly inactivating A-type potassium channels. May contribute to I(To) current in heart and I(Sa) current in neurons. Channel properties are modulated by interactions with other alpha subunits and with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     every third position.
SIMILARITY: Belongs to the potassium channel family. D (Shal)
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Name=1; Synonyms=Long;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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AAM46843.1; -.
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                                                                             Cytoplasmic (Potential).
Segment S1 (Potential).
Segment S2 (Potential).
Cytoplasmic (Potential).
Segment S3 (Potential).
Segment S4 (Potential).
Cytoplasmic (Potential).
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  (pore-forming) (Potential).
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RESULT
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DT 01
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SITE
VARSPLIC
                                                                                               QBWN02;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Voltage-gated potassium channel Kv4.3 long form.
Mustela putorius furo (Ferret)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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                                                                                                                                                                                           Q8WN02
 MEDLINE=21896086; PubMed=11897837; Patel S.P., Campbell D.L., Morales
                         SEQUENCE FROM TISSUE=Heart;
                                                                                        Mammalia;
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                                                                                        Carnivora;
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96.2%;
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  Morales
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Pred. No. 3.2
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Selectivity filter (By similarity).
Missing (in isoform 2).
/FTId=VSP_008830.
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RESULT
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REMBL; AF454388; AAL51038.1; -.

REMBL; AF544388; AAL51038.1; -.

REMBL; AF454388; AAL51038.1; -.

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Q9PTD3;
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J. Physiol. 539:649-656(2002).
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                                                                                                                                                                                                                           GLTTT
                                                                                                                                                                                                                                                                                                                                                                                                                            AQKKARLARIRVAKTGSSNAYLHSKRNGLLNEALELTGTPEEEHMGKTTSLIESQHHHLL
                                                                                                                                                                                                                                                  GLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDG
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                                                                                                                                   LRPNCKTSQITTAIISIPTPPALTPEGESRPPPASPGPNTNIPSIASNVVKVSAL
                                                                                                                                                                                                                                                                                                               HCLEKTTGLSYLVDDPLLSVRTSTIKNHEFIDEQMFEQNCMESSMQNYPSTRSPSLSSHP
                                                                                                                                                                                                                                                                                                                                                                                                       AQKKARLAR IRVAKTGSSNAYLHSKRNGLLTEALELMGTPEEEHVGKSTSL I ESQHHHLL
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                         PRELIMINARY;
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AA; 7
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Pred. No. 5e-1
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                        -----NHEFIDEOMFEONCMESSMONYPSTRSPSLSSHP
                         PRT;
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                       658
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Query Match
Best Local S
Matches 605
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R HSSP; Q63881; 1S6C.

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0008076; C:voltage-gated potassium channel com

R GO; GO:0005249; F:voltage-gated potassium channel act

GO; GO:0005249; F:voltage-gated potassium channel act

R GO; GO:0005249; F:voltage-gated potassium channel act

R GO; GO:0006812; P:cation transport; IEA.

R GO; GO:0006813; P:potassium ion transport; IEA.

R GO; GO:0006813; P:potassium ion transport; IEA.

R InterPro; IPR000210; BTB POZ.

R InterPro; IPR0005821; Ion_trans.

R InterPro; IPR001622; K+channel_pore.

R InterPro; IPR003968; KV_channel.

R InterPro; IPR003991; K_channel.

R InterPro; IPR003991; K_channel.

R InterPro; IPR003991; K_channel.

R InterPro; IPR003991; K_tetra.

R InterPro; IPR00391; K_tetra.

R InterPro; IPR003975; Shal_channel.

R Pfam; PF02214; K_tetra; 1.

Pfam; PF02214; K_tetra; 1.

Pfam; PF02214; K_tetra; 1.

Pfam; PF02214; K_tetra; 1.

Pfam; PF02214; K_tetra; 1.

PRINTS; PR01491; KVCHANNEL.

R PRINTS; PR01491; KYCHANNEL.

R PRINTS; PR01491; SHALCHANNEL.

R PRINTS; PR01491; SHALCHANNEL.

R PRINTS; PR01497; SHALCHANNEL.

PRINTS; PR01497; SHALCHANNEL.

PRINTS; PR01497; SHALCHANNEL.

PRINTS; PR01497; SHALCHANNEL.

PRINTS; PR01497; SHALCHANNEL.

PRINTS; PR01497; SHALCHANNEL.

PRINTS; PR01497; SHALCHANNEL.

PRINTS; PR01497; SHALCHANNEL.

PRINTS; PR01586 MA; 0F8743D4AF8B12AB CRC64
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Submitted
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Potassium channel Kv4.3.
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361
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YTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQNQRADKR
                                                                                                                                                                                                                            PSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPASFW
                                                                                                                                                                            EYLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGAFVTLRVFRVFRIFK
                                                                                                                                                      EYLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGAFVTLRVFRVFRIFK
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White Leghorn;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.2%;
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13,
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Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 3126; DB 2;
Pred. No. 3.1e-187;
9; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasianinae;
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2A8 CRC64;
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                                                                                                   Query Match
Best Local S
Matches 556
                                                                                                                                                                                                  Lautermilch N.J., Spitzer N.C.;

Lautermilch N.J., Spitzer N.C.;

Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databas

R EMBL; U89265; AAB94379.1; -.

RSSP; Q63881; 136C.

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0008076; C:voltage-gated potassium channel com

R GO; GO:0008076; C:voltage-gated potassium channel act

GO; GO:0005249; F:voltage-gated potassium channel act

R GO; GO:0005249; F:voltage-gated potassium channel act

R GO; GO:0006812; P:cation transport; IEA.

GO; GO:0006813; P:potassium ion transport; IEA.

R GO; GO:0006813; P:potassium ion transport; IEA.

R InterPro; IPR003131; P:potassium ion transport; IEA.

R InterPro; IPR0031622; K+channel pore.

InterPro; IPR0031622; K+channel.

InterPro; IPR003966; KV43channel.

R InterPro; IPR003131; K_ctran.

InterPro; IPR003131; K_ctran.

R InterPro; IPR003131; K_ctran.

R InterPro; IPR003975; Shal_channel.

R InterPro; IPR003975; Shal_channel.

R Pfam; PF002214; K_ctran; 1.

R Pfam; PF002214; K_ctran; 1.

R Pfam; PF00214; KVCHANNEL.

R PRINTS; PR01491; KVCHANNEL.

R PRINTS; PR01491; KVCHANNEL.

R PRINTS; PR01491; KVCHANNEL.

R PRINTS; PR01255; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             057662;
057662;
01-JUN-1998
                                                                                                                                                    Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potassium channel xKv4.3.
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NCBI_TaxID=8355
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               61
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                                                                                                                    Similarity
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YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF
                                                         MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKRQDELIVLNVSGRRFQTWRTTLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGLRPNCKTSQITTAIISIPTPPALTPEGESRPPPASPGPNTNI-PSITSNVVKVSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HHGLTTSCCSRRHKKTTHLPNSSVPATRLRSMQELSTIHTQCSEQPSLTTSRSSLNMKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPGLTTTCCSRRSKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAQKKARLARIRVAKTGSSNAYLHSKRNGLLNEALELTG-TPEEEHMGKTTSLIESQHHH
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                                           MASGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKKQDEVIILNVSGRRFQTWRTTLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                   85.6%;
                                                                                                      39;
                                                                                                   Score 2843.5; DB 2;
Pred. No. 1.4e-169;
9; Mismatches 39;
                                                                                                                                                              Transmembrane; Tra
73F5CF339C6A0F47
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                                                                                                                                                              Transport.
F47 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complex;
                                                                                                      Indels
                                                                                                                                Length
                                                                                                                                  659;
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                                                                                                     27;
                                                                                                   Gaps
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XX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
XX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
XA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
XA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
XA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
XA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
XA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
XA Babak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
XA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
XA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
XA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                     Q7ZW36
Q7ZW36;
Q7ZW36;
Q1-JUN-2003 (TrEMBLrel. 2
Q1-JUN-2003 (TrEMBLrel. 2
Q1-QCT-2003 (TrEMBLrel. 2
Potassium voltage-gated c
                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=AB; TISSUE=
                                                                                                                                                                                                                                                                                                           ORFNames=zgc:55306;
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24, Last sequence update)
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channel, Shal-related family,
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REMEL; BCO45304; A,AH45304.1; -.

REMEL; BCO45304; C:integral to membrane; IEA.

RGO; GO:0016021; C:integral to membrane; IEA.

RGO; GO:0008076; C:voltage-gated potassium channel complex;

RGO; GO:0005515; F:protein binding; IEA.

RGO; GO:0005516; F:voltage-gated potassium channel activity;

RGO; GO:0005249; F:voltage-gated potassium channel activity;

RGO; GO:0006812; P:cation transport; IEA.

RGO; GO:0006813; P:potassium ion transport; IEA.

RINTERPRO; IPR000210; BTB POZ.

RINTERPRO; IPR000210; BTB POZ.

RINTERPRO; IPR001622; K+channel pore.

RINTERPRO; IPR001622; K+channel.

RINTERPRO; IPR003968; KV_channel.

RINTERPRO; IPR003968; KV_channel.

RINTERPRO; IPR003131; K_tetra.

RINTERPRO; IPR003131; K_tetra.

RINTERPRO; IPR003975; Shal_channel.

RPINTS; PR01518; KV43CHANNEL.

RPINTS; PR01491; KV43CHANNEL.

RRINTS; PR01491; KVCHANNEL.

RRINTS; PR01497; SHALCHANNEL.

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Best Local 9
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Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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360
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                TIVIMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQNQRADKRR
                                                                                                                                              ### MALVFYYVTGFFIALSVITNVVETVPCGYMPNQRDVPCGERYTEAFFCMDTACVMIFTVE
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2590; DB 2;
Pred. No. 9.7e-154;
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Best Local S
Matches 488
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A Patel S.P., Strauss H.C.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databas
R EMBL; AY147192; AAN39878.1; -.
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0008076; C:voltage-gated potassium channel com
R GO; GO:0005515; F:protein binding; IEA.
R GO; GO:0005249; F:voltage-gated potassium channel act
R GO; GO:0006812; P:cation transport; IEA.
R GO; GO:0006813; P:potassium ion transport; IEA.
R InterPro; IPR000210; BTB_POZ.
R InterPro; IPR0005821; Ion_trans.
R InterPro; IPR001622; K+Channel_pore.
R InterPro; IPR003968; KV_channel.
R InterPro; IPR003968; KV_channel.
R InterPro; IPR00391; K_channel.
R InterPro; IPR003975; Shal_channel.
R InterPro; IPR003975; Shal_channel.
R Pfam; PF00520; Ion trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00520; Ion trans; 1.
Pfam; PF02214; K tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01517; KV42CHANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01497; SHALCHANNEL.
                                                                                                                                                                                                                                                                                                                               PRINTS; PR01517; KV42CHANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01497; SHALCHANNEL.
SMART; SM00225; BTB; 1.
Ion transport; Ionic channel; T
SEQUENCE 630 AA; 70565 MW;
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Q8HYZ1;
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Voltage-gated potassium channel Kv4.2.
Mustela putorius furo (Ferret)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mustela.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    538
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                                                                                                                                                                                                                        488;
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13
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                                                                                                                                                                                                                                                   Similarity
RYPDTLLGSSERDFFYHPETQQYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDEELA
                           RYPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELA
                                                                                                                                         MAAGVAAWLPEARAAAIGWMPVANCPMPLAPADKNKR-QDELIVLNVSGRRFQTWRTTLE
                                                                                                            MAAGVAAWLPFARAAAIGWMPVASGPMPAPPRQERKRTQDALIVLNVSGTRFQTWQDTLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLLHCLEKTTNHEFVDERLYEQGYLQTALQNFPS-QSPSLSSEEGITGTCCSRRPKKNIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIPTPPA----LTPEGESRPPPASPGPNTNIPSITSNVVKVSVL
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                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                              76.2%;
                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                     Score 2530; DB 2;
Pred. No. 5.4e-150;
3; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                 Transmembrane; Transport. DA4CFD16998A9842 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   630
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P59995;
29-MAR-2004
                                                                                                                                      MEDLINE=22117972; PubMed=12122138;
Sanchez D., Lopez-Lopez J.R., Perez-Garcia M.T.,
Obeso A., Ganfornina M.D., Gonzalez C.;
"Molecular identification of Kv alpha subunits to
oxygen-sensitive K(+) current of chemoreceptor c
                                                                                                                                                                                                                                                                                                                                                                                                      29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Potassium voltage-gated channel subfamily D m
potassium channel subunit Kv4.2).
                  -
                                                                                                           carotid body.";
J. Physiol. (Lond.) 542:369-382(2002).
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=New Zealand white;
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                      SEQUENCE OF
                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                   Rae J.L.;
                                                                                                                                                                                                                                                                                                                                                                                             Name=KCND2;
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9986;
  regulatory subunits.
SUBUNIT: Homotetramer or heterotetramer with Associates with the regulatory subunits KCNII
                                             FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly inactivating A-type potassium channels. May contribute to I(To) current in heart and I(Sa) current in neurons. Channel properties are modulated by interactions with other alpha subunits and with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVEYLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGAFVTLRVFRVFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STLALVFYYVTGFFIAVSVITNVVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPTPPVTTPEGDDRPESPEYSGG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRRAQKKARLARIRAAKTGSANAYMQSKRNGLLSNQLQ-SSEDEQAFVSKSGSSFETQHH
                                                                                                                                                                                                                                                    (MAY-2002)
                                                                                                                                                                                                                     15-614 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                              Lagomorpha;
 the regulatory
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                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                   TISSUE=Cornea
                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                     FUNCTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                              Leporidae; Oryctolagus
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    KCNIP1,
                                                                                                                                                                                                                      TISSUE
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                                                                                                                                          that contribute cells of the rak
                 KCND1
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                                                                                                                                                                                                                     SPECIFICITY
  KCNIP2,
                                                                                                                                                                                                                                                                                                                                                                                                                         (Voltage-gated
                 and/or
    KCNIP3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF493547; AAM46841.1; ...
InterPro; IPR005821; Ion trans.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR003131; K_tetra.
InterPro; IPR005820; M+channel_nlg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00520; Ion trans; 1.
Pfam; PF02214; K tetra; 1.
Ion transport; Ionic channel;
Potassium; Potassium channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and FINC (By similarity)
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Detected in brain frontal cortex.
DOMAIN: The segment S4 is probably the voltage-sensor characterized by a series of positively charged amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
SIMILARITY: Belongs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     every third position. PTM: Phosphorylated on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subfamily.
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                          181
                                                                            121
                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF508735; AAM46929.1; -. AF493547; AAM46841.1: -
                                                                                                                                                                                                                                  489;
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                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                            MAAGVAAWLPFARAAAIGWMPVANCPMPLAPADKNKR-QDELIVLNVSGRRFQTWRTTLE
                                     STLALVFYYVTGFFIAVSVITNVVETVPCGTVPGS-KELPCGERYSVAFFCLDTACVMIF
                                                                                          FYGILPEIIGDCCYEEYKDRKRENAERLMDDNDSENNQES-MPSLSFRQTMWRAFENPHT
                                                                                                                                           RYPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELA
                                                                                                                                                                               MAAGVAAWLPFARAAAIGWMPVASGPMPAPPRQERKRTQDALIVLNVSGTRFQTWQDTLE
  TVEYLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTNNEDVSGAFVTLRVFRVFRI
                                                                                                                            RYPDTLLGSSERDFFYHPETQQYFFDRDPDIFRHILNFYRTGKLHYPRHECISAYDEELA
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                                                                                                                                                                                                                                                                                         Cytoplasmic (Potential).
Selectivity filter (By similarity).
Phosphothreonine (By similarity).
Phosphoserine (By similarity).
Phosphothreonine (By similarity).
Phosphothreonine (By similarity).
Phosphothreonine (By similarity).
Phosphoserine (By similarity).
E-> K (in Ref. 2).
K-> R (in Ref. 2).
                                                                                                                                                                                                                                69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        serine and threonine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic (Potential).
Segment S1 (Potential).
Segment S2 (Potential).
Cytoplasmic (Potential).
Segment S3 (Potential).
Segment S4 (Potential).
                                                                                                                                                                                                                                           Score 2524;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                           Segment S5 (Potential).
Segment H5 (pore-forming)
Segment S6 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multigene family; Pho
Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               potassium
                                                                                                                                                                                                                                                                                   5981C87A5E4C41D1 CRC64;
                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                          DB 1;
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RESULT 11

KCD2_MOUSH
ID KCD2_AC
AC Q920\
AC Q920\
DT 29-MI
DT 29-MI
DT 05-JI
DE POTAG
GN Name=
OS MUS 11
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STRAIN=C57BL/6J; TISSUE=Mesonephros, and Olfactory bulb;
STRAIN=C57BL/6J; PubMed=12466851; DOI=10.1038/nature01266;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
                                                                                                                                                        cDNAs identified by screening of terminal sequences of cDNA cloner randomly sampled from size-fractionated libraries.";

DNA Res. 9:179-188(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugar
Hashimoto K.;
"Isolation of full-length cDNA clones from mouse brain of Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Swiss Webster; TISSUE-Heart ventricle; Tanaka H., Janzen K., Winkfein R.J., Fiset C., Claranaka H., Winkfein R.J., Fiset C., Claranaka H., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                            MEDLINE=22353125; PubMed=12465718;
Okazaki N., Kikuno R., Ohara R., Inamoto S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
                                                                                                                                                                                                                                                                       Okazaki N., Kikuno R., Oha
Ohara O., Koga H.;
"Prediction of the coding
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Osada N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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use heart K+
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RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Ravasi T., Reed J.C., Semple C.A., Setou M., Shimada K.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Yasunishi A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Harashizaki V., Waterston R., Lander E.S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobo Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Břadt D., Brusic V., Chothia C., Corbani L.E., Cousi Balla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERACTION WITH KCND3 AND KCNIP2.
MEDLINE=21906624; PubMed=11909823;
DOI=10.1161/01.RES.0000012664.05949.E0;
GOD W., Li H., Aimond F., Johns D.C., Rhodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20497051; PubMed=11040264; Varga A.W., Anderson A.E., Adams J. "Input-specific immunolocalization Kv4.2 in the mouse brain."; Learn. Memory 7:321-332(2000).
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[7]
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                                                                                                                                                                                                                                                                                                                                                                                                               Circ. Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nerbonne J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Role of heteromultimers in
                                                                                                                                                                                       and FLNC (By similarity).

SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: Detected in brain, especially in
                                                                                                                                                                                                                                                         regulatory subunits.

SUBUNIT: Homotetramer or heterotetramer with KCND1 and/or KCND3.

SUBUNIT: Homotetramer or heterotetramer with KCNIP1, KCNIP2, KCNIP3 a

RESOCIATES with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 a

KCNIP4. Interacts with DPP6, DLG4 and FREQ. Interacts with FLNA
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FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly inactivating A-type potassium channels. May contribute to I(To) current in heart and I(Sa) current in neurons. Channel properties are modulated by interactions with other alpha subunits and with
                                                                    Subfamily. CAUTION: R
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BL; AB045326; BAA97986.1; ALT_FRAME.
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Selectivity filter (By similar:
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V -> A (in Ref. 2).
S -> R (in Ref. 3).
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Segment S2 (Potential).
Cytoplasmic (Potential).
Segment S3 (Potential).
Segment S4 (Potential).
Cytoplasmic (Potential).
Cytoplasmic (Potential).
Segment S5 (Potential).
Segment H5 (pore-forming)
Segment H5 (Potential).
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Pred. No. 1.5e-149;
8; Mismatches 70;
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RESULT 12

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ROBERDS S.L., Tamkun M.M.;
RCloning and tissue-specific expression of five voltage-gated "Cloning and tissue-specific expressed in rat heart.";
Proc. Natl. Acad. Sci. U.S.A. 88:1798-1802(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KCD2 RAT STANDARD; PRT; 630 AA. Q63881; Q00090; Q99249; Q9-MAR-2004 (Rel. 43, Created) 29-MAR-2004 (Rel. 43, Last sequence update) 29-MAR-2004 (Rel. 45, Last annotation update) 25-CCT-2004 (Rel. 45, Last annotation update) Potassium voltage-gated channel subfamily D member potassium channel subunit Kv4.2) (Shall) (RK5).
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MEDLINE=92000693; PubMed=1840649;
Baldwin T.J., Tsaur M.-L., Lopez (
"Characterization of a mammalian of sensitive K+ channel.";
Neuron 7:471-483 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
NCBI TaxID=10116;
 INTERACTION WITH KCNIP1 AND FREQ.
MEDLINE=21532927; PubMed=11606724;
Nakamura T.Y., Pountney D.J., Ozait
Coetzee W.A.;
                                                                                                                              INTERACTION WITH KCNIP1; KCNIP2 AND KCNIP3.
MEDLINE=20140134; PubMed=10676964; DOI=10.1038/35000592;
An W.F., Bowlby M.R., Betty M., Cao J., Ling H.-P., Mendoza G.,
Hinson J.W., Mattsson K.I., Strassle B.W., Trimmer J.S., Rhodes
"Modulation of A-type potassium channels by a family of calcium
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND TISSUE SPECI
STRAIN-Sprague-Dawley; TISSUE-Heart;
MEDLINE-91156694; PubMed-1705709;
Roberds S.L., Tamkun M.M.;
                                                                                                                                                                                                                                                                                                                                                                                  Neuron
[2]
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Rodentia;
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Sciurognathi; Muridae;
                     Ozaita
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ; DOI=10.1016/0896-6273(91)90299-F;
G.A., Jan Y.N., Jan L.Y.;
cDNA for an inactivating voltage-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE
                  DOI=10.1073/pnas.221168498;
ta A., Nandi S., Ueda S., Ru
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, Murinae; Rattus.
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                      Rudy
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PDB; 1S6C;
InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUTAGENESIS OF 627-VAL--LEU-630, AND INTERACTION WITH DLG4.
MEDLINE=22037905; PubMed=11923279; DOI=10.1074/jbc.M109412200;
Wong W., Newell E.W., Jugloff D.G.M., Jones O.T., Schlichter L.C.;
"Cell surface targeting and clustering interactions between heterologously expressed PSD-95 and the Shal voltage-gated potassium channel, Kv4.2.";
                                                                                                                                                                                                                                                               use by non-profit institumodified and this statement entities requires a license
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                                                                                                                                                                                                      EMBL;
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Proc. Natl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              role
                                                                                                                                                                                                                                           send an email to license@isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPP6, DLG4 or FREQ may increase cell surface expression. TISSUE SPECIFICITY: Highly expressed in heart and througout the brain, with similar levels in cortex and hypothalamus, and muchigher levels in hippocampus, dentate gyrus and the habenular nucleus of the thalamus. Detected at similar levels in heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Homotetramer or heterotetramer was associates with the regulatory subunits with FLNA and FLNC (By with DPP6, DLG4 and FREQ. SUBCELLULAR LOCATION: Integral membrane is subcellular to carrior.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Subfamily. CAUTION: F
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SIMILARITY:
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                                                                                                                                                                                                                                                                                                                              European
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                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collable on the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in the fied and this statement is not removed. Usage by and for confident and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                 frameshift
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JU0271; JU0271.
1S6C; X-ray; B=1-30.
p; IPR005821; Ion trans.
p; IPR001622; K+channel pore.
p; IPR003091; K_channel.
p; IPR003131; K_tetra.
p; IPR004055; KV42channel.
p; IPR003968; Kv_channel.
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ano N., Ohya S., 7
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ion of CALP/KChIP4, a novel
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in heart and througout the
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Pfam; PF02214; K_tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01517; KV42CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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InterPro; IPR003975; Shal_channel.
Pfam; PF00520; Ion_trans; 1.
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PR01497; SHALCHANNEL.
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FWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQNQRAD
                                                                                                                                                                    FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPAS
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n; Potassium; Potassium channel;
Transport; Voltage-gated channel
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75.8%;
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Phosphothreonine (By similarity).
Phosphoserine (By similarity).
Phosphothreonine (By similarity).
Phosphothreonine (By similarity).
Phosphoserine (By similarity).
Phosphoserine (By similarity).
Missing: Abolishes interaction with DI
                                                                                                                                                                                                                                                                                                                                                                                                           69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Segment S1 (Potential).
Segment S2 (Potential).
Cytoplasmic (Potential).
Segment S3 (Potential).
Segment S4 (Potential).
Cytoplasmic (Potential).
Cytoplasmic (Potential).
Segment S5 (Potential).
Segment H5 (pore-forming)
Segment H5 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                           Score 2519; Di
Pred. No. 2.6e
9; Mismatches
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Segment S6 (E
Segment S6 (E
Cytoplasmic (E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          channel; Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (pore-forming) (Potential).
                                                                                                                LSGVLVIALPVPVIVSNFSRIYHQNQRAD
                                                                                                                                                                                                                                                                                                                                                                                                                      6e-149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential)
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                                          LSSHPGLTTTCCSRRSKKTTH
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                                SSOOGVTSTCCSRRHKKSFR
                                                                                                                                                                                                  VSGAFVTLRVFRVFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transport;
                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                          479
                                                                                            477
                                                                                                                420
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RESULT

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MEDLINE 223616434; PubMed=12690205; DOI=10.1126/science.1083423; RA Scherer S.W., Cheung J., MacDonald J.R., Osborne L.R., Nakabayashi K., RA Herbrick J.-A., Carson A.R., Parker-Katiraee L., Skaug J., Khaja R., RA Zhang J., Hudek A.K., Li M., Haddadd M., Duggan G.E., Fernandez B.A., RA Kanematsu E., Gentles S., Christopoulos C.C., Choufani S., RA Kanematsu E., Gentles S., Christopoulos C.C., Choufani S., RA Kwasnicka D., Zheng X.H., Lai Z., Nusskern D., Zhang Q., Gu Z., Lu F., RA Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C., RA Zeesman S., Nowaczyk M.J., Teshima I., Chitayat D., Shuman C., RA Weksberg R., Zackai E.H., Grebe T.A., Cox S.R., Kirkpatrick S.J., RA Weksberg R., Zackai E.H., Grebe T.A., Cox S.R., Kirkpatrick S.J., RA Belloni E., Shaffer L.G., Pober B., Morton C.C., Gusella J.F., RA Bruns G.A.P., Korf B.R., Quade B.J., Ligon A.H., Ferguson H., Higgins A.W., Leach N.T., Herrick S.R., Lemyre E., Farra C.G., Kim H.-G., Summers A.M., Gripp K.W., Roberts W., Szatmari P., RA Kim H.-G., Summers A.M., Gripp K.W., Roberts W., Szatmari P., RA Armengol L., Pujana M.A., Estivill X., Wilson M.D., Koop B.F., Tosi S., Moore G.E., Boright A.P., Zlotorynski E., Kerem B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99061682; PubMed=9843794; Kong W., Po S., Yamagishi T., Ashen M.D., Stetten "Isolation and characterization of the human gene further diversity by alternative mRNA splicing."; Am. J. Physiol. 275:H1963-H1970(1998).
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29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Potassium voltage-gated channel subfamily D
potassium channel subunit Kv4.2).
Name=KCND2; Synonyms=KIAA1044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KCD2 HUMAN
Q9NZV8; O95012;
29-MAR-2004 (Re
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which co for large proteins in vitro.";
DNA Res. 6:197-205(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhu X.-R., Wulf A., Schwarz M., Isbrandt D., Pongs O., "Characterization of human Kv4.2 mediating a rapidly-inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., TISSUE SPECIFICITY, MEDLINE=20017432; PubMed=10551270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kikuno R., Nagase T., Ishikawa K.-I., Hirosawa M., Miyajima
Tanaka A., Kotani H., Nomura N., Ohara O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Gene structures and expression profiles potassium channels mediating A-type curre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isbrandt D., Leicher
Michel U., Sauter K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20195625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., FUNCTION,
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hannels 6:387-400(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=10729221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Pongs O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              current.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          currents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of three human KCND (Kv4) ents I(TO) and I(SA).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIFICITY
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                                                                                                                                                      InterPro; IPR0039/5,
InterPro; IPR0039/5,
Pfam; PF00520; Ion_trans; 1
Pfam; PF02214; K_tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01517; KV42CHANNEI
PRINTS; PR01491; KVCHANNEI
PRINTS; PR01491; KVCHANNEI
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PRINTS; PRO151.,
PRINTS; PRO1491; KVCHANNEL.
PRINTS; PRO1497; SHALCHANNEL.
Ion transport; Ionic channel; Multigene f
Ion transport; Jonic channel; Potassium
Cytoplasmi
Cytoplasmi

Transport; Voltage-gated DOMAIN 1 183
TRANSMEM 184 204

Segment

S1

transport;

family; Phosphorylation;

InterPro; InterPro;

[nterPro; interPro; nterPro;

InterPro;

; Shal\_cm\_

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"Localization and enhanced current density of the channel by interaction with the actin-binding prot J. Neurosci. 20:8736-8744 (2000).
                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents
                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF121104; AAD22053.1;
EMBL; AB028967; BAA82996.2;
EMBL; AJ010969; CAB56841.1;
EMBL; AF166008; AAF65618.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kroisel P.M., Petek E., Oscier D.G., Mould S.J., Doehner K., Rommens J.M., Vincent J.B., Venter J. Mural R.J., Adams M.D., Tsui L.-C.; "Human chromosome 7: DNA sequence and biology.";
                                                                                                                                                                                                                                   Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20556633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTAGENESIS OF 601-PRO--PRO-604, WITH FLNA AND FLNC.
                                                                                                                                                                                                             H-InvDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement
                                                                                                                                                                   nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulatory subunits.

SUBUNIT: Homotetramer or heterotetramer with KCND1 and/or KCND3. Associates with the regulatory subunits KCNIP1, KCNIP2, KCNIP3 a KCNIP4. Interacts with DPP6, DLG4 and FREQ (By similarity). Interacts with FLNA and FFLNC.

SUBCELLULAR LOCATION: Integral membrane protein. Detected in dendrites in cultured hippocampal neurons.

TISSUE SPECIFICITY: Highly expressed throughout the brain. Expression is very low or absent in other tissues.

DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Pore-forming (alpha) subunit of voltage-gated rapidly inactivating A-type potassium channels. May contribute to I(To) current in heart and I(Sa) current in neurons. Channel properties are modulated by interactions with other alpha subunits and with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
SIMILARITY: Belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subtamily.
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                                                                                                                                                                                                                                                         AF142568;
Q16968; 1
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AC004888;
                                                                                                                                                                                                                                         HGNC
o; IPR005821; Ion_trans.
o; IPR001622; K+channel_pore.
o; IPR003091; K_channel.
o; IPR0031311; K_tetra.
o; IPR004055; KV42channel.
o; IPR003968; Kv_channel.
o; IPR003968; Kv_channel.
o; IPR003975; Shal_channel.
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R GO; GO:0018076; C:voltage-gated potassium channel complex;

R GO; GO:0008515; F:protein binding; IEA.

R GO; GO:0005219; F:voltage-gated potassium channel activity

R GO; GO:0005812; P:cation transport; IEA.

R GO; GO:0006813; P:potassium ion transport; IEA.

R GO; GO:0006813; P:potassium ion transport; IEA.

R Pfam; PF00520; Ion trans; 1.

Pfam; PF00520; Ion trans; 1.

Pfam; PF00150; FCHANNEL.

R PFINTS; PR0169; FCHANNEL.

R PRINTS; PR01517; KV42CHANNEL.

R PRINTS; PR01491; KV42CHANNEL.

R PRINTS; PR01497; SHALCHANNEL.

R SMART; SM00225; BTB; 1.

SMART; SM00225; BTB; 1.

SEQUENCE 632 AA; 70982 MW; 147C92979F2297D9 CRC64;
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                                                                                                                                                                                                                                      FWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQNQRAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HHLLHCLEKTTNHEFIDEQMFEQNCMESSMQNYPSTRSPSLSSHPGLTTTCCSRRSKKTT
                                                                                               KRRAQKKARLARIRVAKTGSSNAYLHSKRNGLLNEALELTGTPEEE-HMGKTTSLIESQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVEYLLRLLAAPSRYKFVRSVMSIIDVVAIMPYYIGLVMTDNEDVSGAFVTLRVFRVFRI
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                                                                                                                                                                                                                                                                                                                                                                          PKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMYYAEKGSSASKFTSIPAA
                                                                                                                                                                                                                                                                                                                                                                                                                    FKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSIPAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.8%;
76.2%;
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20, Last sequence update)
26, Last annotation update)
potassium channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 2517; DB 2;
; Pred. No. 3.5e-149;
62; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         632
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RESULT
KCD1_MC
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                                                                                                                                                                                A Chazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Maglott D.R., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
Yang Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato.
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Minaki A., Soshino K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino K., Waterston R., Lander E.S., Rogers J.,
RA Hara A., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pak M.D., Ba
Salkoff L.;
                INTERACTION WITH KCNIP1.
MEDLINE=21316019; PubMed=11423117; DOI=10.1016/S0014-5793(01)02560-1;
Nakamura T.Y., Nandi S., Pountney D.J., Artman M., Rudy B.,
Coetzee W.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KCD1 MOUSE STANDARD; PRT; 651 AA. 003719; Q8CC68; Q9-MAR-2004 (Rel. 43, Created) 29-MAR-2004 (Rel. 43, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Potassium voltage-gated channel subfamily D m potassium channel subunit Kv4.1) (mShal).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                "Analysis of the mouse transcriptome 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                     Birney E., Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 145-647 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22354683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "mShal, a subfamily of A-type K+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91239573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Kcnd1;
'Different effects of the Ca(2+)-binding protein, KChIP1, on two Kv4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLPNSNLPATRLRSMOELSTIHIQGSEQPSLTTSRSSLNLKADDGLRPNCKTSQITTAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HHLLHCLEKTTNHEFVDEQLYEESCMEVSTVNRPPSHSPSLSSQQGVTGTCCSRRHKKTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Epididymis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=12466851; DOI=10.1038/nature01266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=2034678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Covarrubias M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        channel cloned from mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Butler A., Ratcliffe A.,
                                                                                                                                                     based
                                                                                                                                                     9
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                                                                                                                                                     functional annotation
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1 Т.,
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Matches
                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003975; Shal channel.
Pfam; PF00520; Ion_trans; 1.
Pfam; PF02214; K tetra; 1.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01516; KV41CHANNEL.
PRINTS; PR01491; KVCHANNEL.
PRINTS; PR01497; SHALCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR005821; Ion trans.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR0030991; K_channel.
InterPro; IPR003131; K_tetra.
InterPro; IPR004054; KV41channel.
InterPro; IPR003968; KV channel.
InterPro; IPR005820; M+channel_nlg.
InterPro; IPR003975; Shal_channel.
                                                                                                                                                          CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                          TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subfamily members, Kv4.1 ar FEBS Lett. 499:205-209(200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M64226; AAA39745.1; -. EMBL; AK033805; BAC28480.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                               Potassium
                                                                                                                                                                                                                                                                                                                                                                           Ion transport; Ionic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
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                                                                                                                                                                                                                                                                                                                                                  Voltage-gated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A39372; A39372.
                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inactivating A-type potassium channels. May contribute to current in the heart and I(Sa) current in neurons. Channel properties are modulated by subunit assembly. SUBUNIT: Homotetramer or heterotetramer with KCND2 and/or Associates with the regulatory subunits KCNIP1, KCNIP2, KCKNIP4 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              every third position.
SIMILARITY: Belongs to the potassium channel family. D (Shal)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Inte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          characterized by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI:96671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q16968; 1A68
                                                                                                                   Similarity
                                                  YPDTLLGSTEKEFFFNEDTKEYFFDRDPEVFRCVLNFYRTGKLHYPRYECISAYDDELAF
  YPDTLLGSSEKEFFYDAESGEYFFDRDPDMFRHVLNFYRTGRLHCPRQECIQAFDEELAF
                                                                                                                                                                                                                                                                                                                                                               channel; Potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            499:205-209(2001)
                                                                                                                                                                                     185
227
248
262
292
292
313
326
365
387
308
                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAR LOCATION: Integral membrane protein.
The segment S4 is probably the voltage-sensor and is rized by a series of positively charged amino acids a
                                                                                                                                                                                                                                                                                                                                                  channe]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kcnd1
                                                                                                                                                           355
71697
                                                                                                                                                                                     205
247
261
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312
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346
407
651
                                                                                                                                                                                                                                                                                                                                                                            channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Kv4.2.";
                                                                                                                                                                   Cytoplasmic (Potential).
Segment S5 (Potential).
Segment H5 (pore-forming) (Potential).
Segment S6 (Potential).
Cytoplasmic (Potential).
Selectivity filter (By similarity).
N-linked (GlcNAc. . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (alpha) subunit of voltage-gated rapidly tassium channels. May contribute to I(To)
                                                                                                     Score 2141.5; DB 1; Pred. No. 1.1e-125; 6; Mismatches 116;
                                                                                                                                                                                                                                                                  Cytoplasmic (Potential Segment S3 (Potential) Segment S4 (Potential)
                                                                                                                                                                                                                                                                                                          Segment S1
Segment S2
                                                                                                                                                                                                                                                                                                                                                               transport;
                                                                                                                                                                                                                                                                                                                                    Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                           Multigene
                                                                                                                                                           -linked (GlcNAc. . .) (P
801DECC3C56C721F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                c (Potential)
(Potential).
                                                                                                                                                                                                                                                                                                                                                             family; Potassium;
Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                         (Potential)
                                                                                                                                                                                                                                                                                                                        (Potential).
                                                                                                         Indels
                                                                                                                                Length
                                                                                                                                                                                                                            (Potential).
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                                                                                                                                  651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a collaboration -
                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCNIP3
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        commercial
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망	8	Дb	Ş	₽	γQ	Db	γQ	В	8	망	Qy	дb	Ş	Дb	Ş	В	ş	뭥	Ş
Db 651 L 651	Qy 636 L 636	Db 592 RDFVAAIISIPTPPANTPD-ESQPSSPSGGGGSGGTPNTTLRNSSLGTPCLLPETVKISS	589 SQITTAIISIPTPPALTPEGESRPPPASPGPNTNI	Db 535 RRVNRRAIRLANSTASVSR-GSMQELDTLAGLRRSPAPQTRSSLNAKPHDSLDLNCDS	QY 530 RR-SKKTTHLPNSNLPATRLRSMQELSTIHIQGSEQPSLTTSRSSLNLKADDGLRPNCKT	Db 476 QQHHHLLHCLEKTTCHEFTDELTFSEALGAVSLGGRTS-RSTSVSSQPMGPGSLFSSCCS	474 SQHHHLLHCLEKTTNHEFIDEQMFEQNCMESSMQNYPSTRSPSLSSHP	Db 420 RADKRRAQQKVRLARIRLAKSGTTNAFLQYKQNGGLEDSGSGDGQMLCVRSRSAFE	415 RADKRRAQKKARLARIRVAKTGSSN	Db 360 PAAFWYTIVTMTTLGYGDMVPSTIAGKIFGSICSLSGVLVIALPVPVIVSNFSRIYHQNQ	355 PASFWYTIVTMTTLGYGDMVPKTIAGKIFGSICSLSGVLV	Db 300 FRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGTSKTNFTSI	Qy 295 FRIFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVMFYAEKGSSASKFTSI	Db 240 LIFTGEYLLRLFAAPSRCRFLRSVMSLIDVVAILPYYIGLFVPKNDDVSGAFVTLRVFRV	235 MIFTVEYLLRLFAAPSRYRFIRSVMSIIDVVAIMPYYIGLVMTN	Db 180 HTSTAALVFYYVTGFFIAVSVIANVVETIPCRGTPRWPSKEQSCGDRFPTAFFCMDTACV	177 HTSTLALVFYYVTGFFIAVSVITNVVETVPCGTVPGSKELPCC	Db 121 YGLVPELVGDCCLEEYRDRKKENAERLAEDEEAEQAGEG-PALPAGSSLRQRLWRAFENP	Qy 121 YGILPEIIGDCCYEEYKDRKRENAERLMDDNDSENNQESMPSLSFRQTMWRAFENP
		TVKISS 650	PSITSNVVKVSV 635	DLNCDS 591	RPNCKT 588	FSSCCS 534	GLTTTCCS 529	SRSAFE 475	TTSLIE 473	IYHQNQ 419	IYHQNQ 414	TNFTSI 359	SKFTSI 354	LRVFRV 299	LRVFRV 294	MDTACV 239	LDTACV 234	RAFENP 179	RAFENP 176

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